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Synthetic Control of Transcription: From Hybrid Promoters to Promoter Engineering to Synthetic Operon Design

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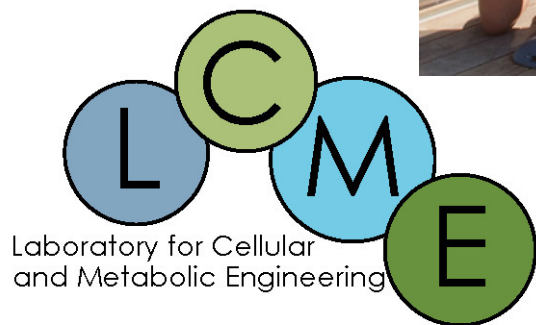
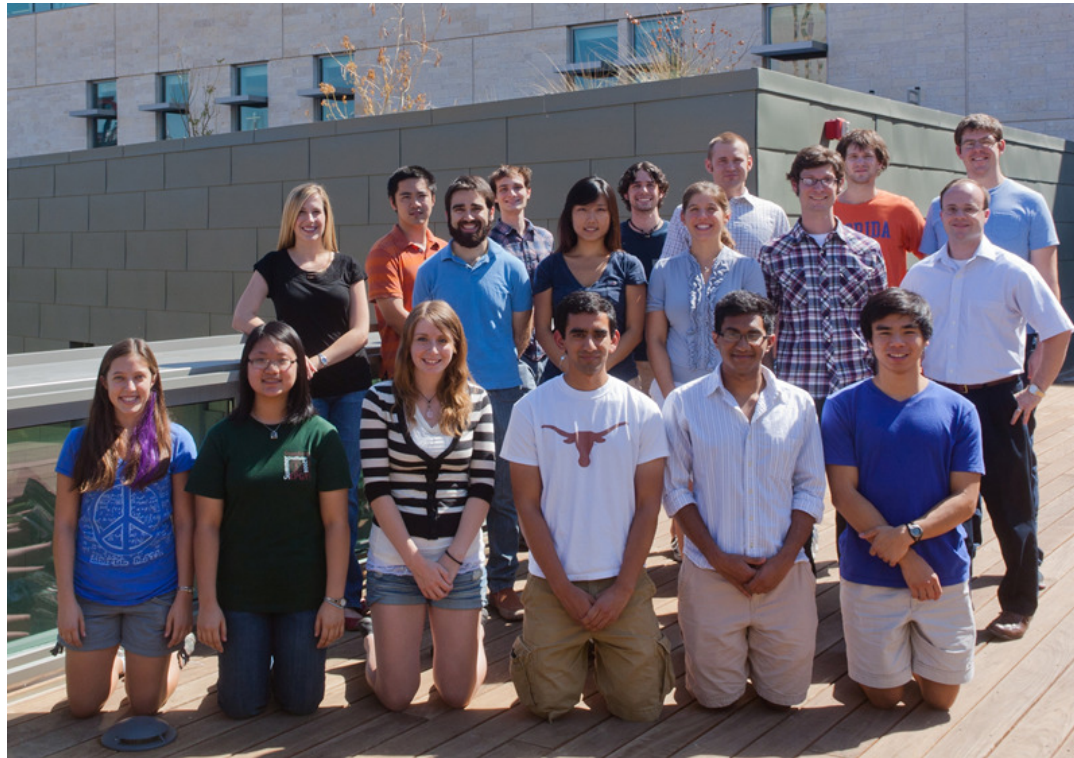
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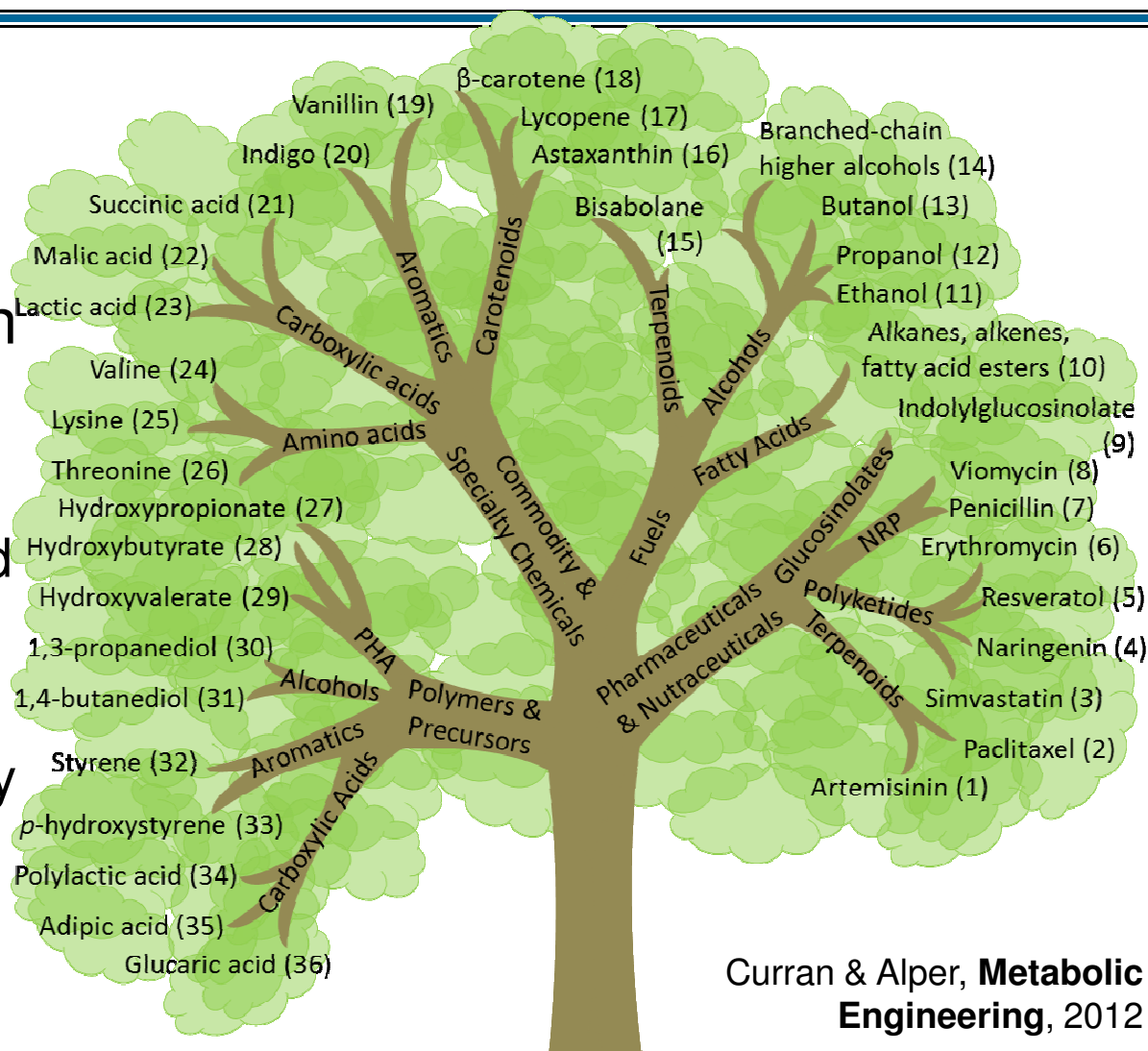
Synthetic control of transcription: From hybrid promoters to promoter engineering to synthetic operon design



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Metabolic Engineering has opened up possibilities...

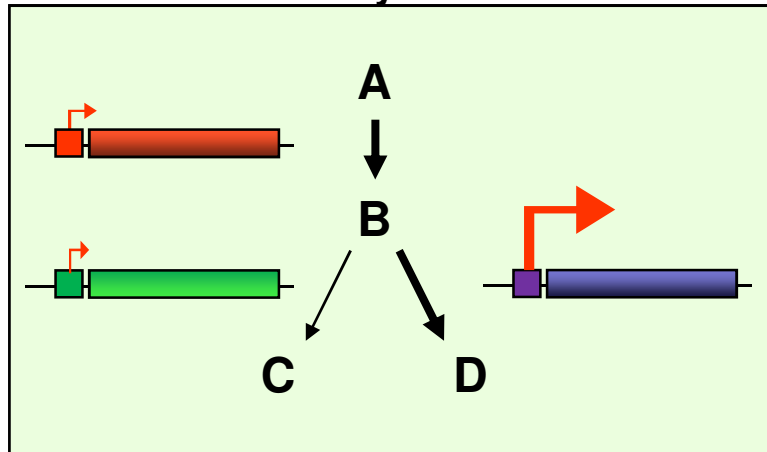
- Metabolic engineering advances have expanded the breath of chemicals produced by cells
 - Pharmaceuticals and Nutraceuticals
 - Fuels
 - Commodity/Specialty Chemicals
 - Polymers and Precursors



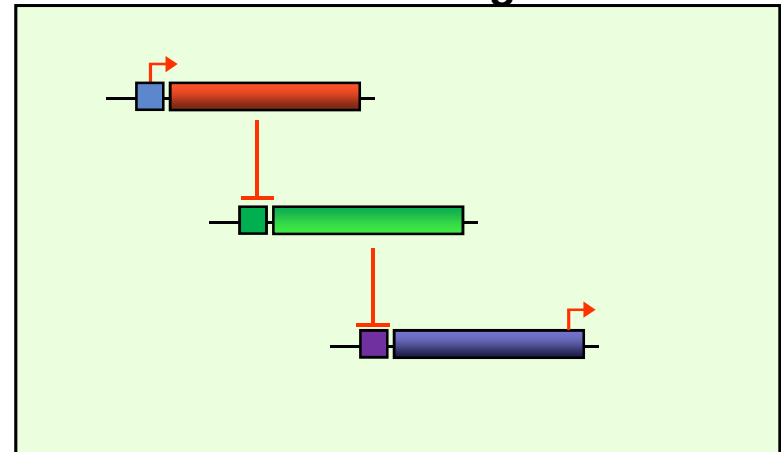
Curran & Alper, **Metabolic Engineering**, 2012

...but, requires synthetic control elements...

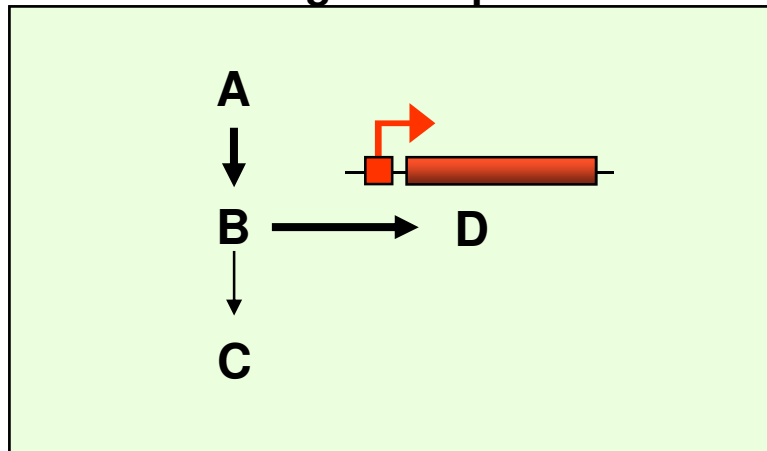
Pathway Control



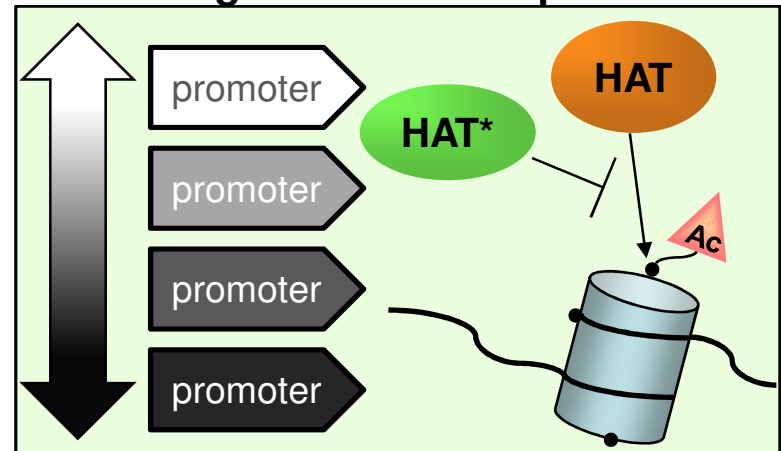
Circuit Design



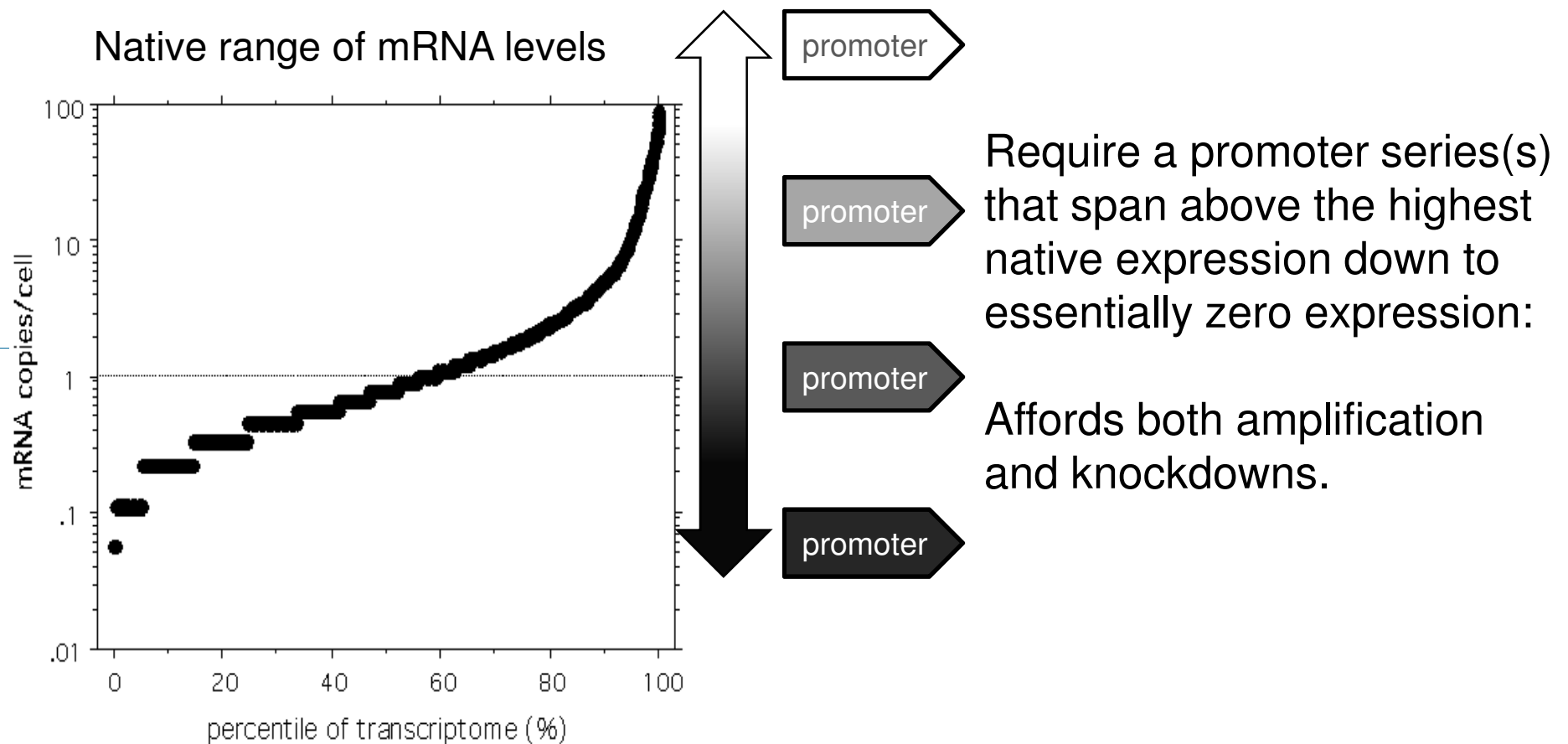
Heterologous Expression



Probing via Graded Expression

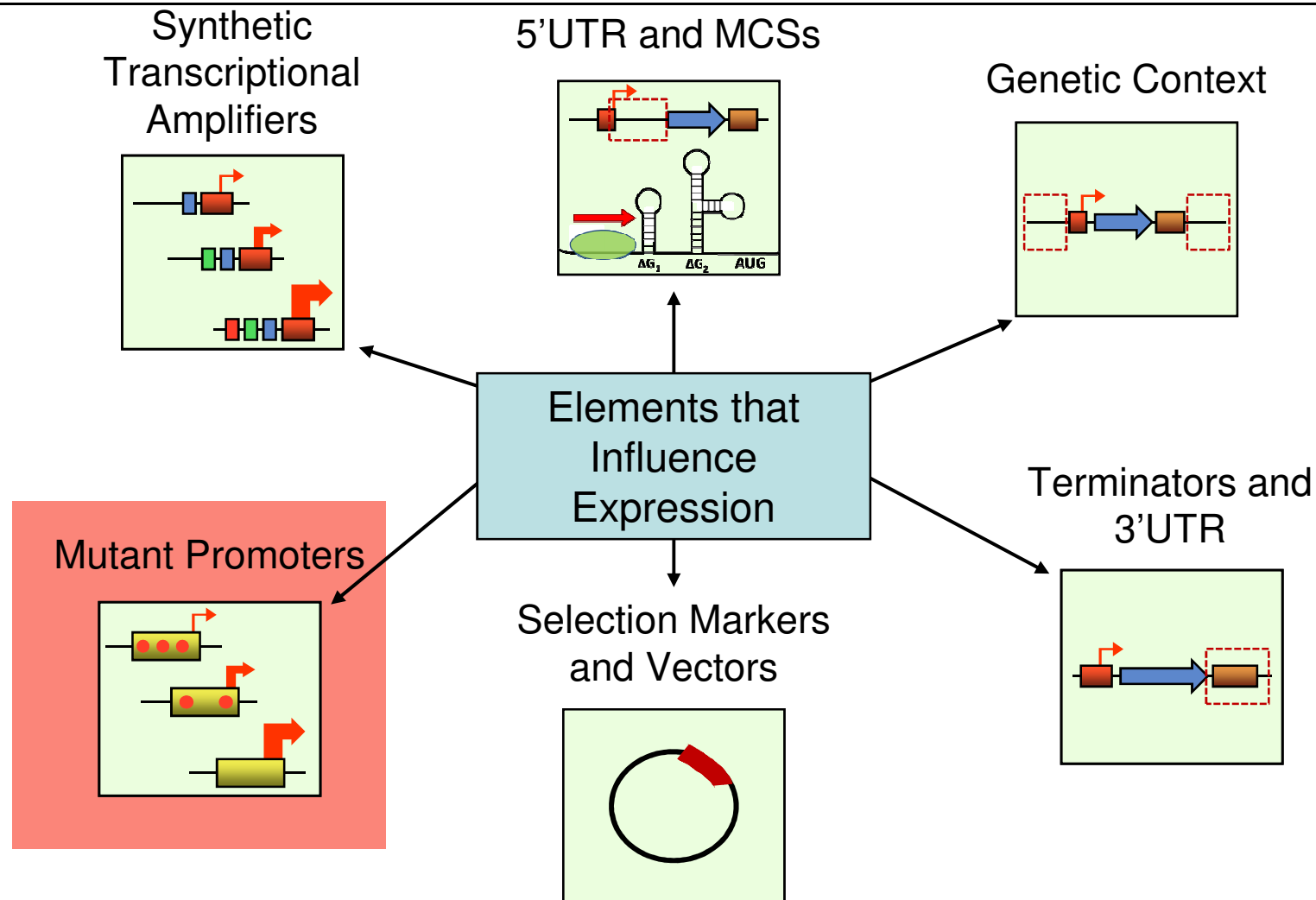


...with a range of expression capacities.



Holstege, et al. (1998), Cell 95:717-728.

Synthetic control of transcription occurs at many levels



Designing novel genetic control elements

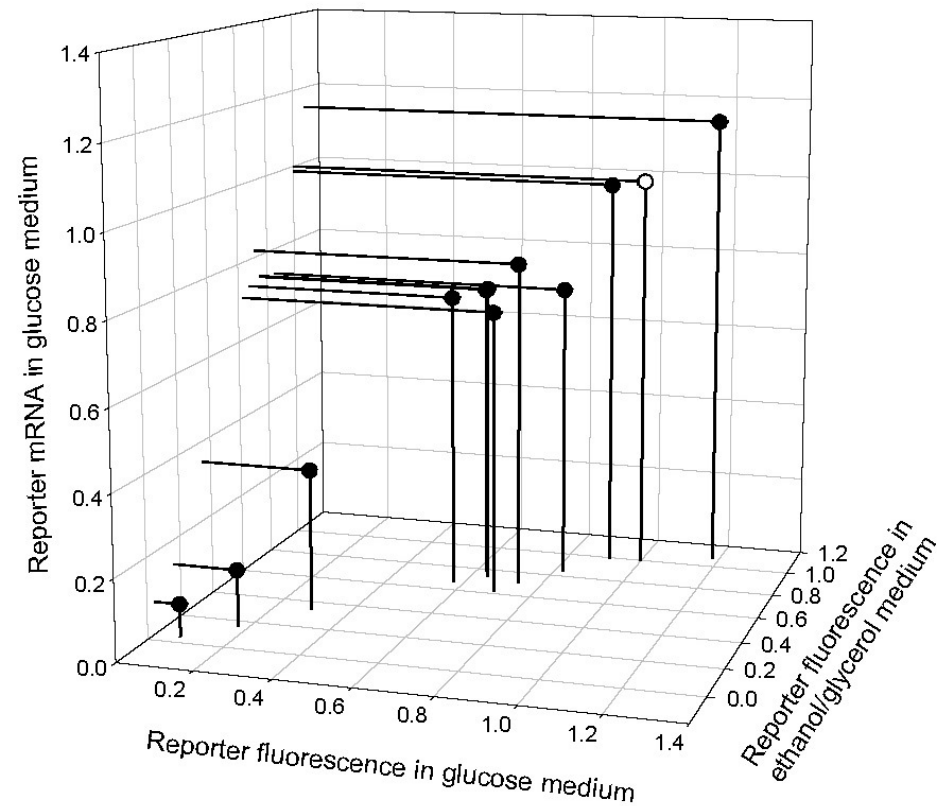
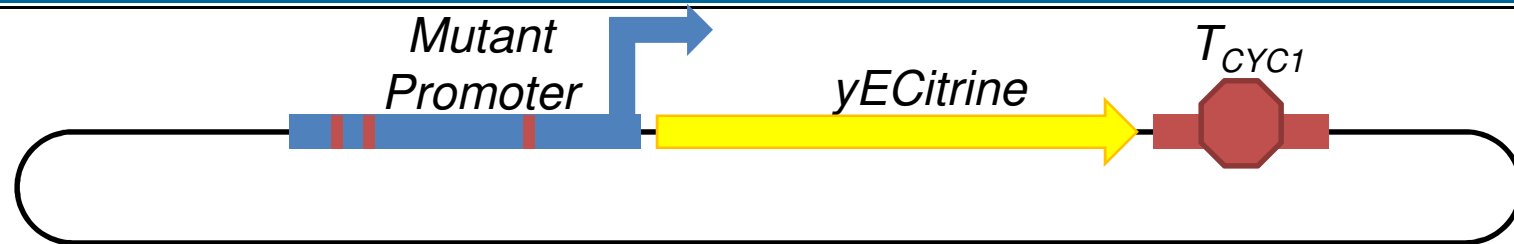
- Promoter Engineering is an effective method for generating a collection of genetic control elements

Prior Promoter engineering example



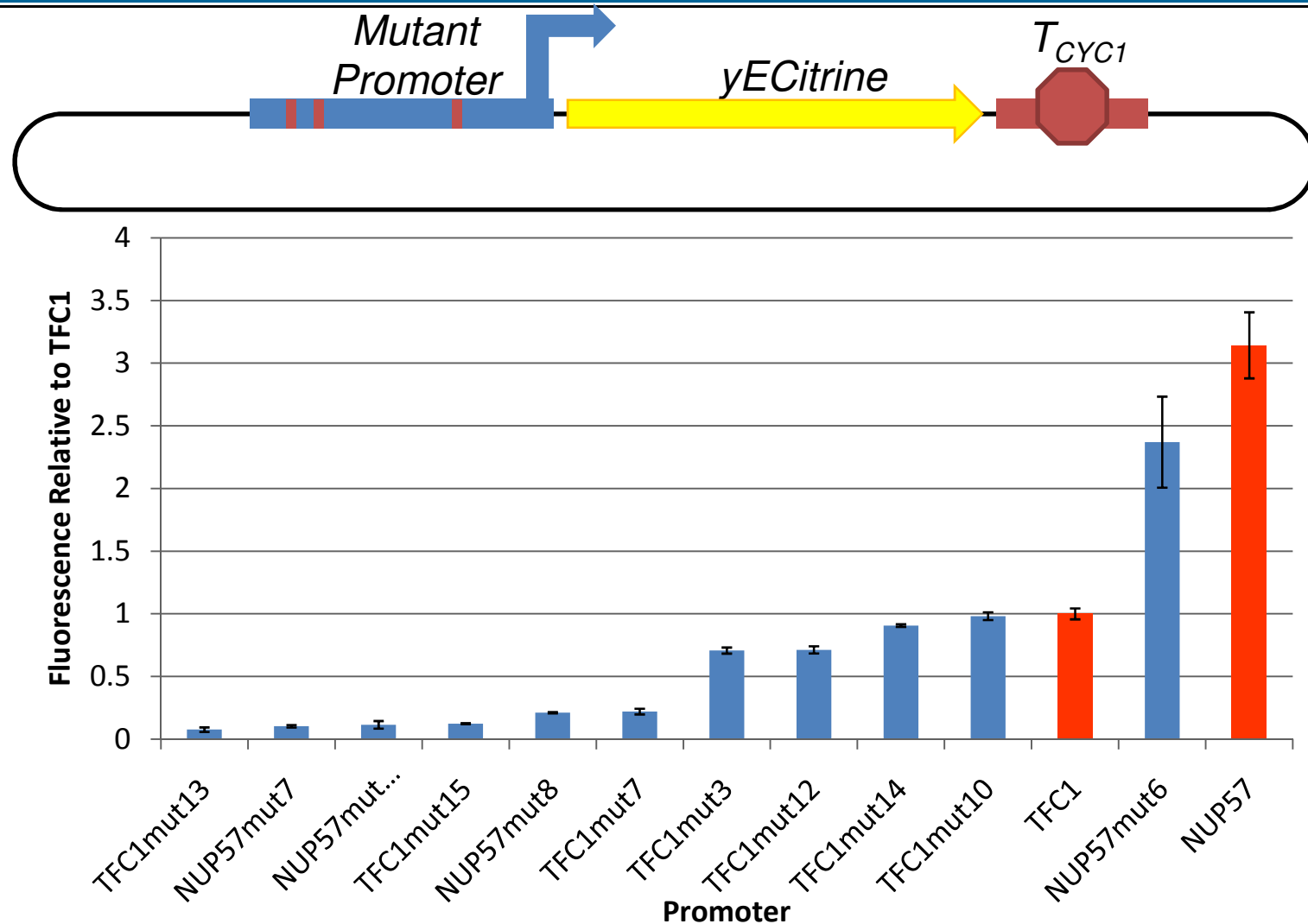
Alper et al. **PNAS**, 2005.

Development of diversified promoters



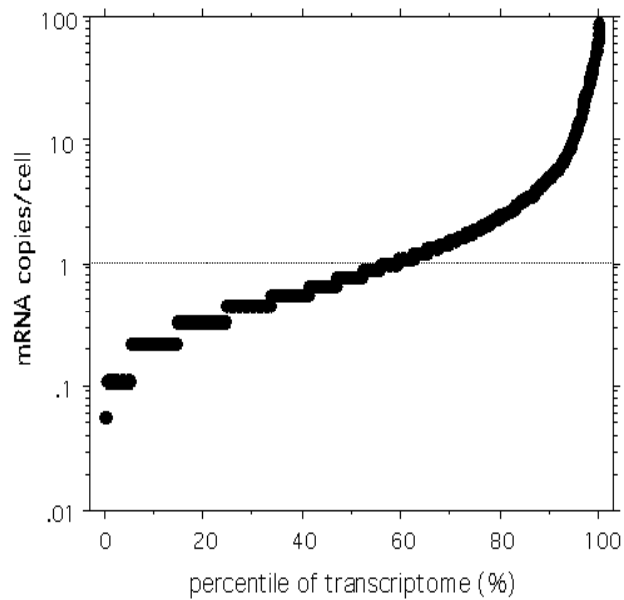
Nevoigt et al. **AEM**, 2006.

Development of novel low-strength promoters

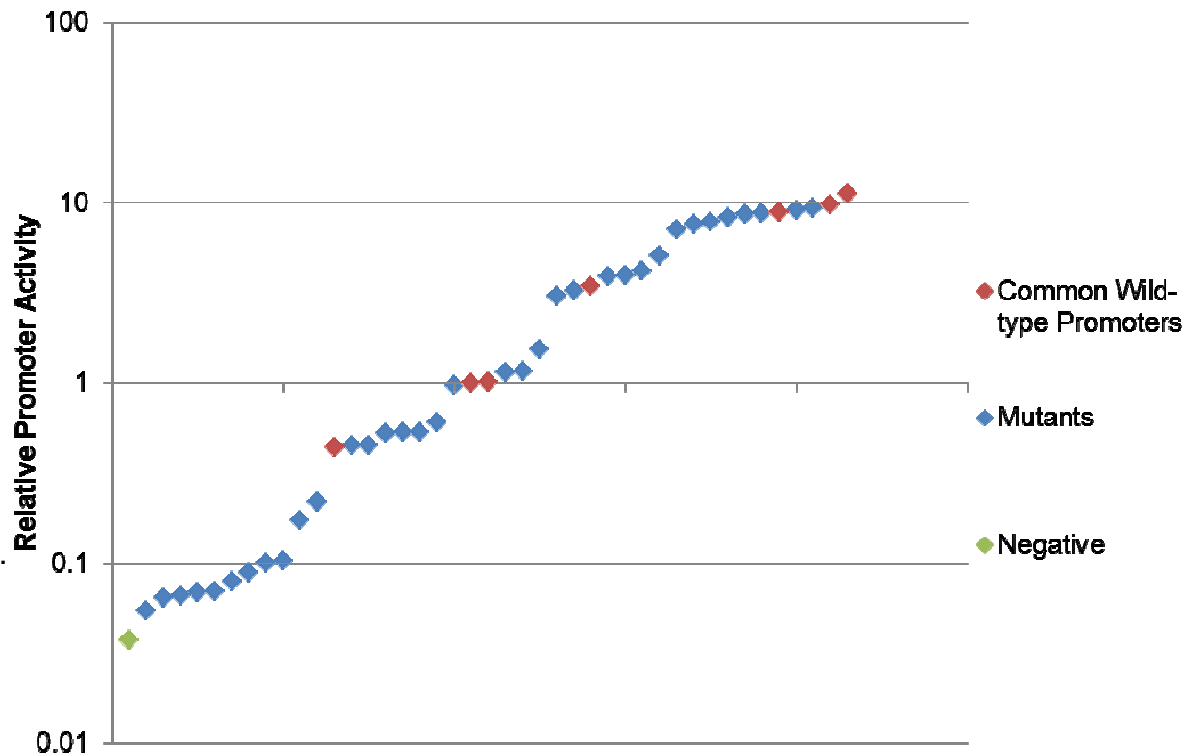


An expanding range of yeast promoters

Native range of mRNA levels



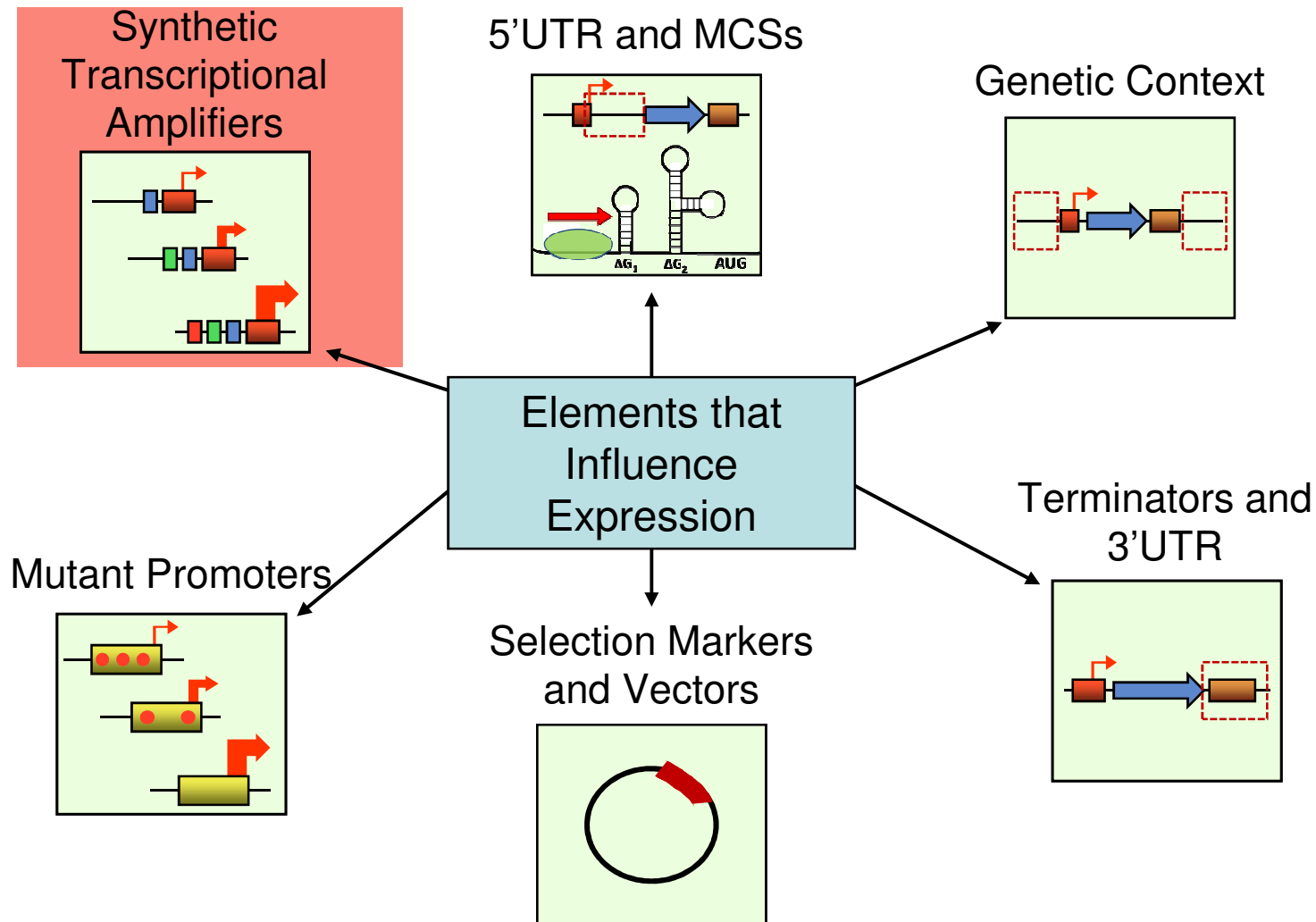
Holstege, et al. (1998), Cell 95:717-728.



Mutant Promoter Libraries

- Promoter engineering via random mutagenesis is effective at creating diversity
- Bias in promoter libraries toward **lower expression capacity**
- Expression range nearly matches “native expression levels”—need more sequence diversity
- Require novel tools for increasing strength of promoters

Synthetic control of transcription occurs at many levels



Promoter Engineering in *Yarrowia lipolytica*



Yarrowia lipolytica is a fully sequenced, oleaginous yeast

Advantages

- Naturally accumulates fatty acids (including linoleic acid) on food source with high C:N ratio
- Semi-developed genetic tools
- Thrives on non-conventional carbon sources

Challenges

- Issues with immature genetic tools and expression levels
 - Low plasmid copy number
 - **Lack of genetic tools**
 - **“Strong” promoters do not readily exist**

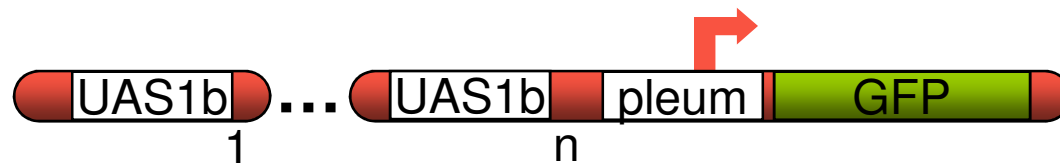
Y. lipolytica Promoter Engineering via tandem UAS sequences



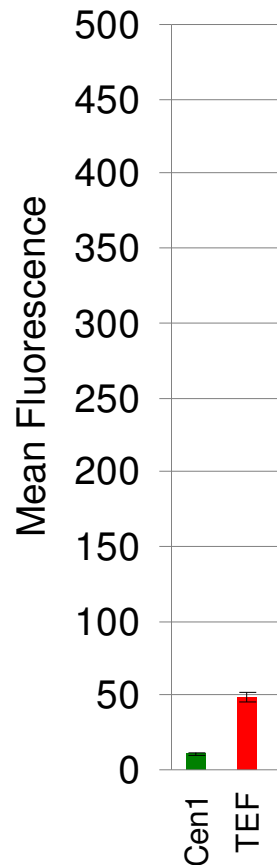
Prior research suggested linking upstream activating sequences (UAS) to a minimal promoter can create function. Analyzed 1 to 4 UAS site.

Madzak et al., *Microbiology*, 1999

We sought to evaluate potential of modulating promoter activity by tandem copies of UAS1b sites ($n = 1$ to 32)



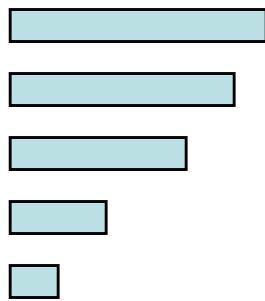
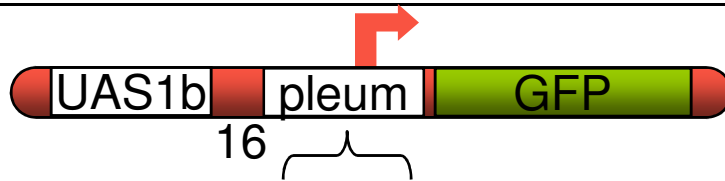
Creation of a strong promoter set in *Y. lipolytica*



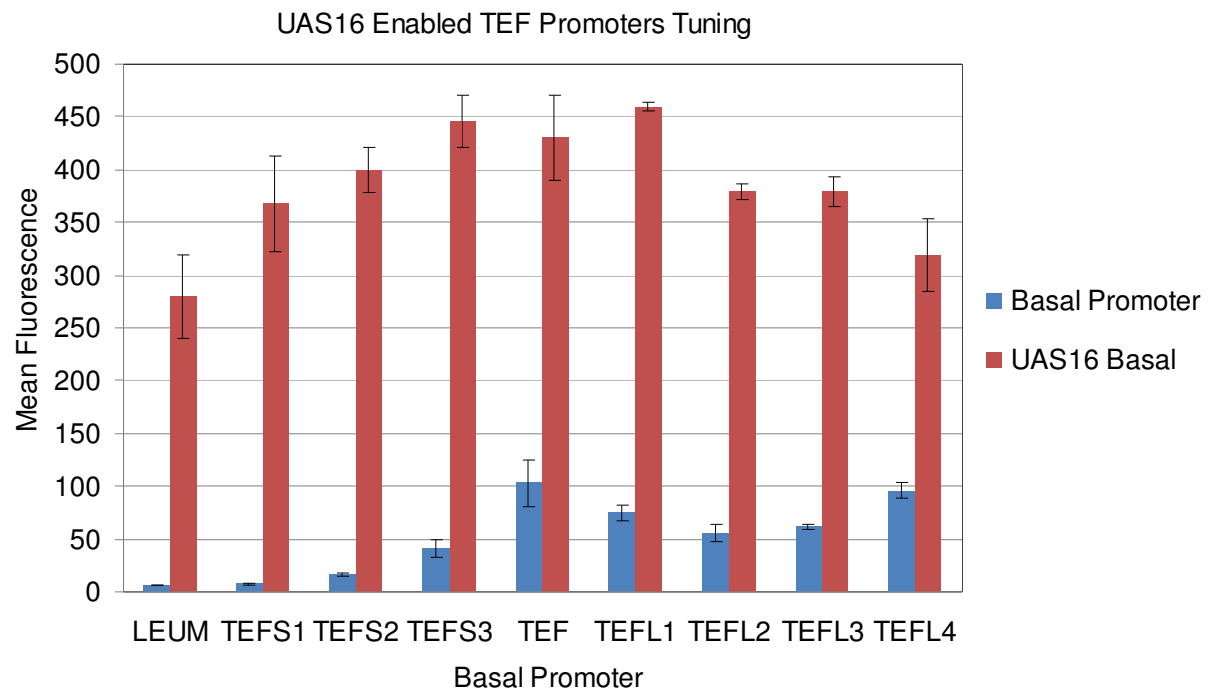
Promoter Construct

Blazeck et al., **AEM**, 77(22), 2011

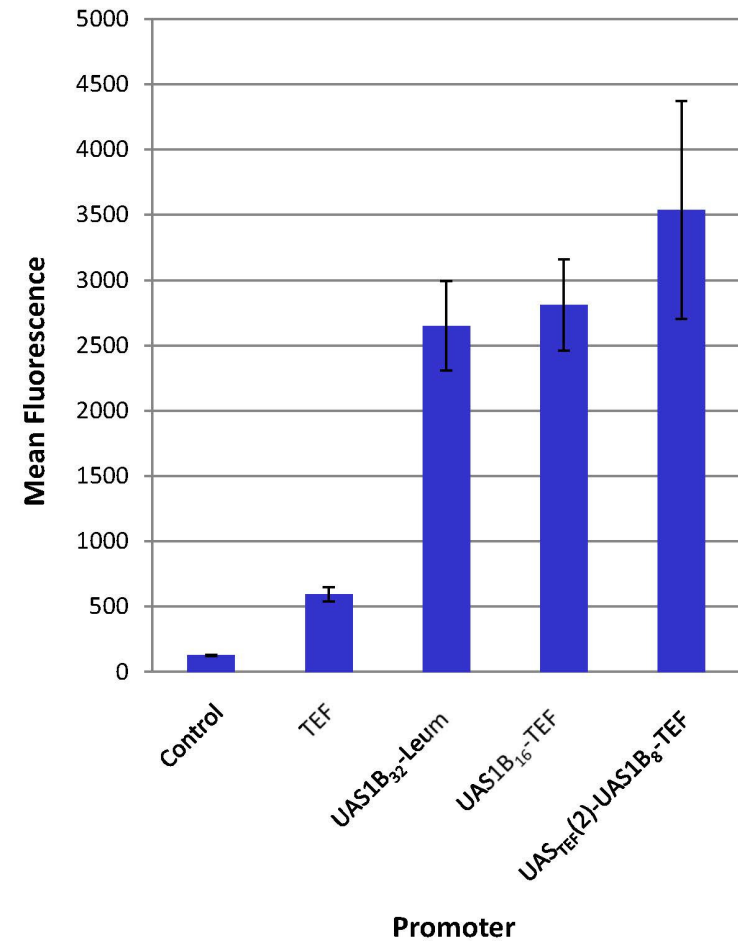
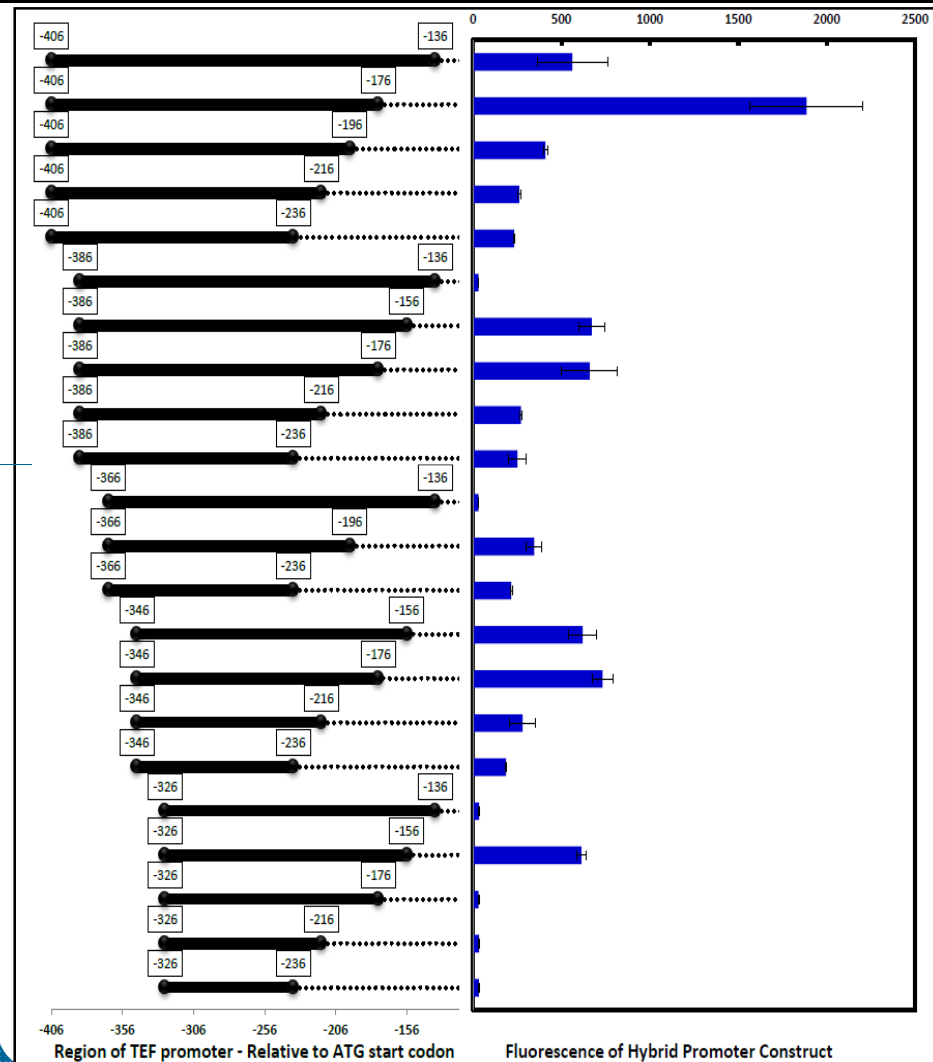
Extension of hybrid promoter strategy



TEF promoter truncation series



Identification and use of a TEF UAS



Blazeck et al., Submitted, **AMB**, 2012

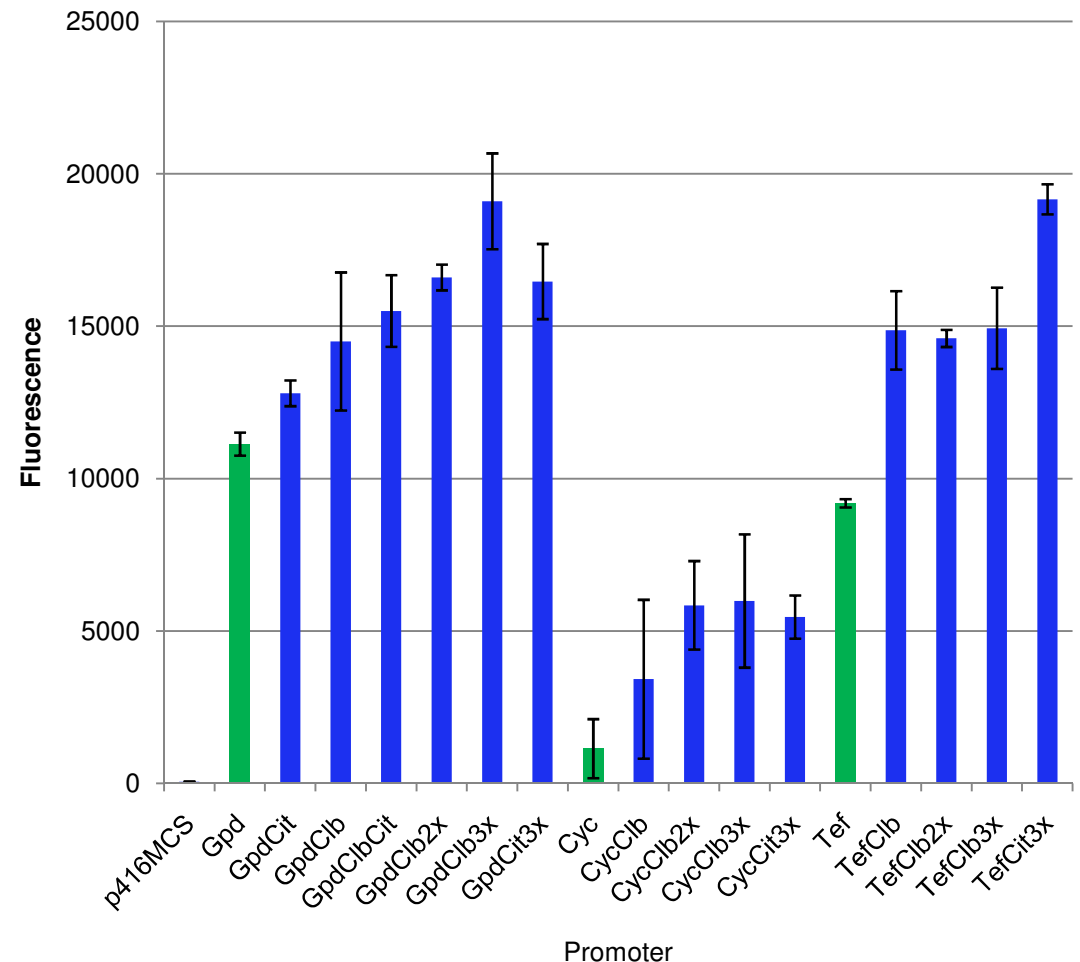
Expanding the hybrid promoter approach to *S. cerevisiae*

UAS Elements



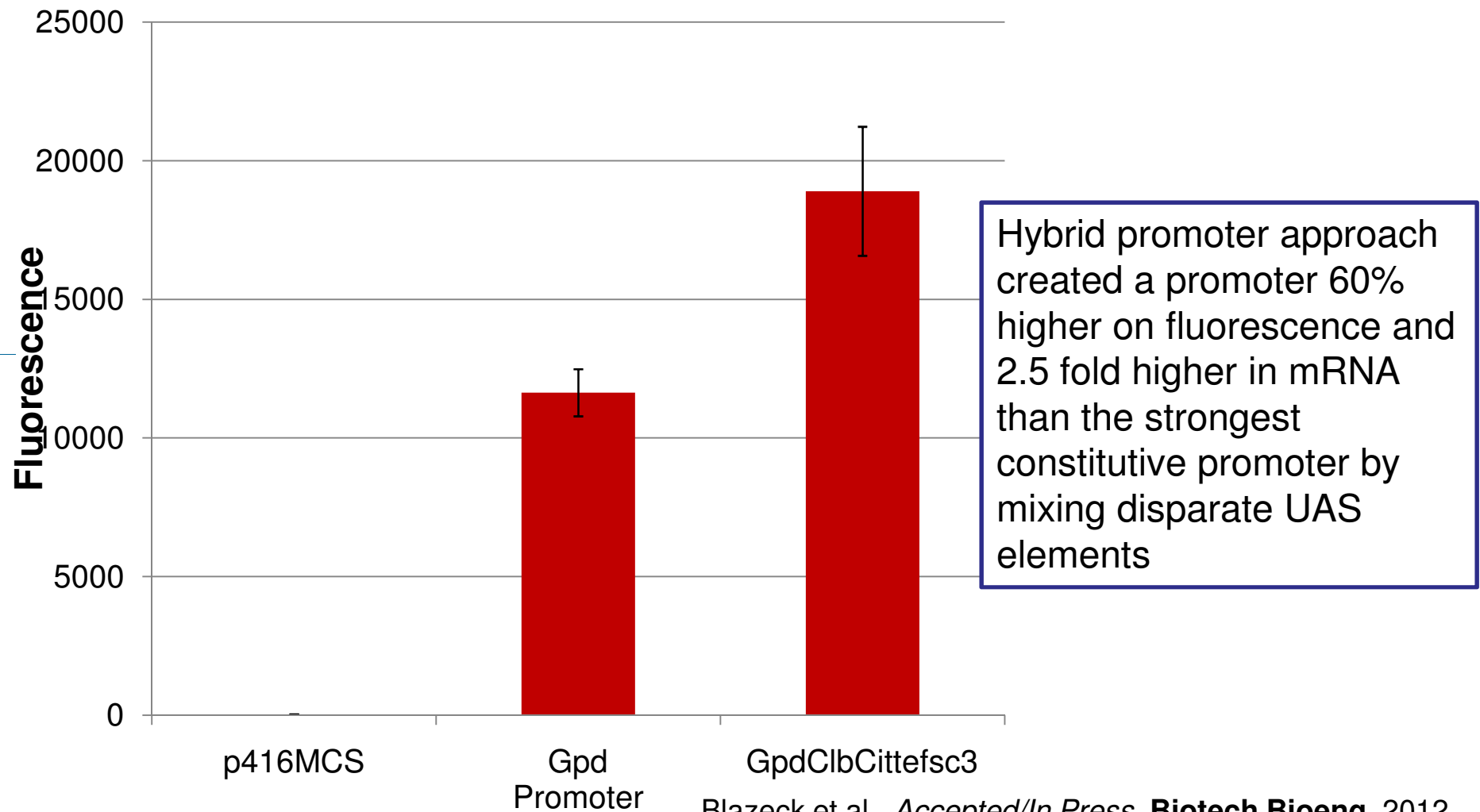
X

Core Promoters

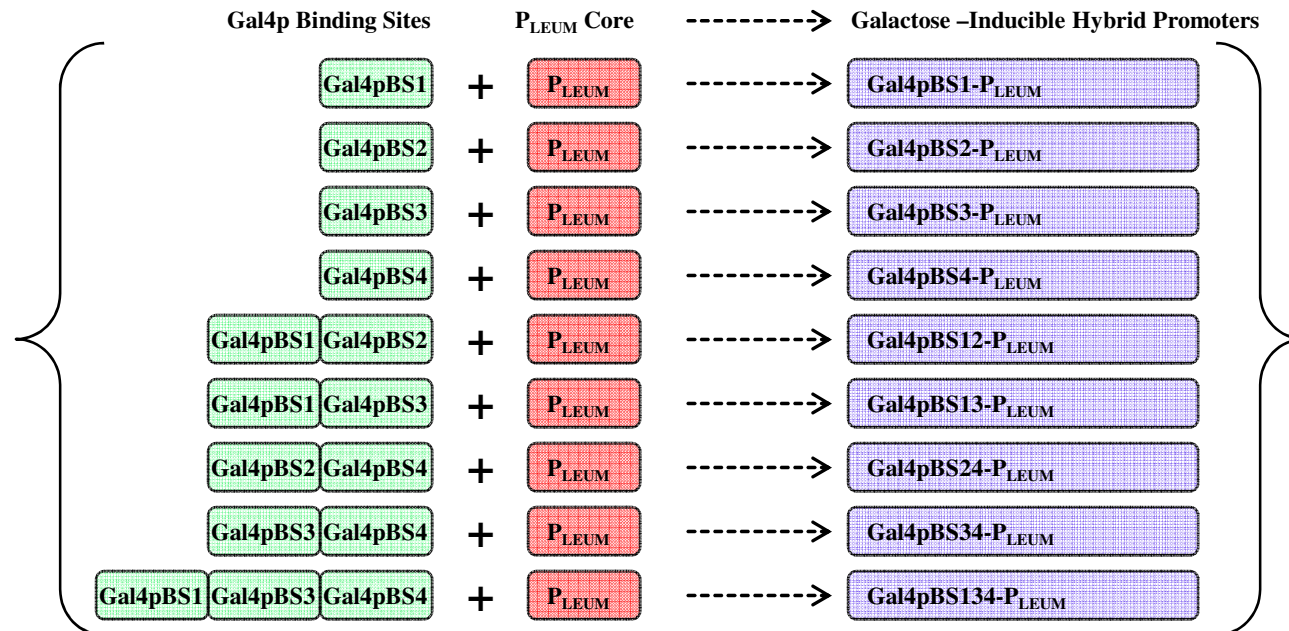
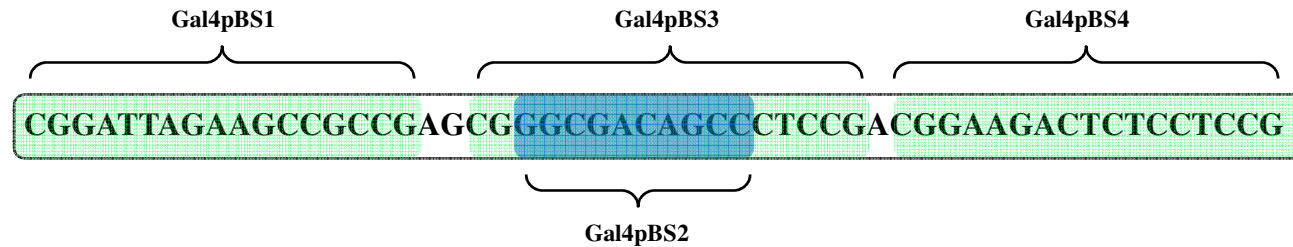


Blazeck et al., *Accepted/In Press, Biotech Bioeng*, 2012

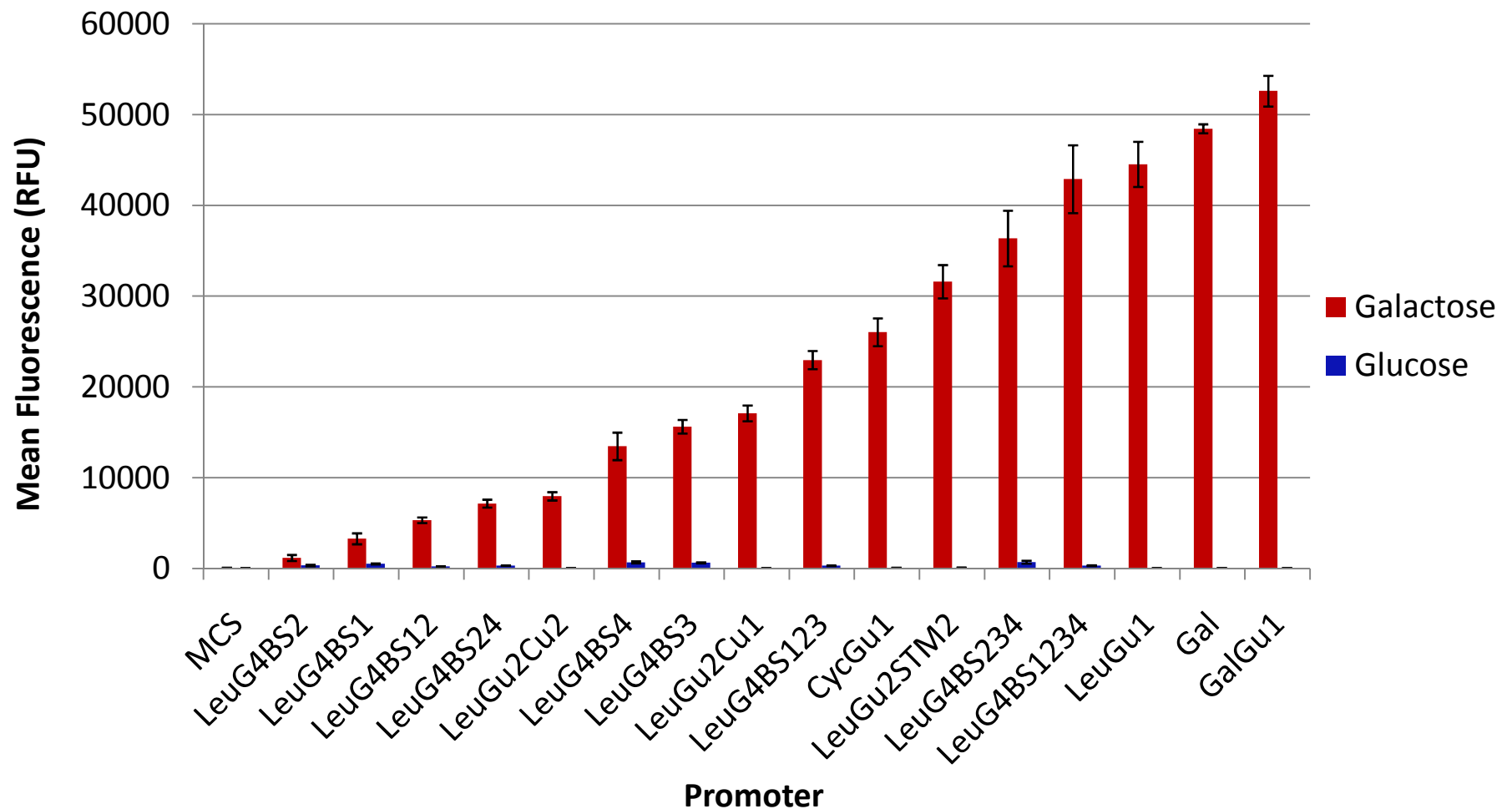
Creating the strongest constitutive promoter



Creating a range of inducible hybrid promoters



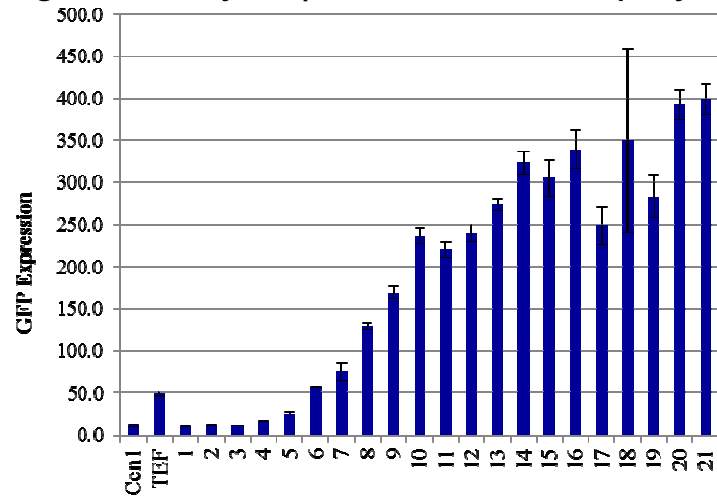
Creating a range of inducible hybrid promoters



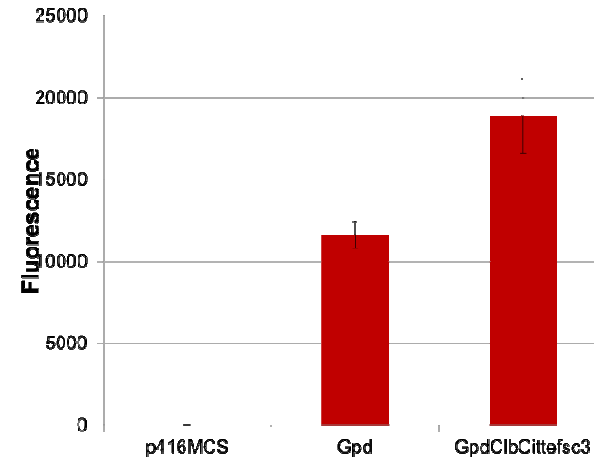
Blazeck et al., *Accepted/In Press*, **Biotech Bioeng**, 2012

Hybrid Promoter Engineering Examples

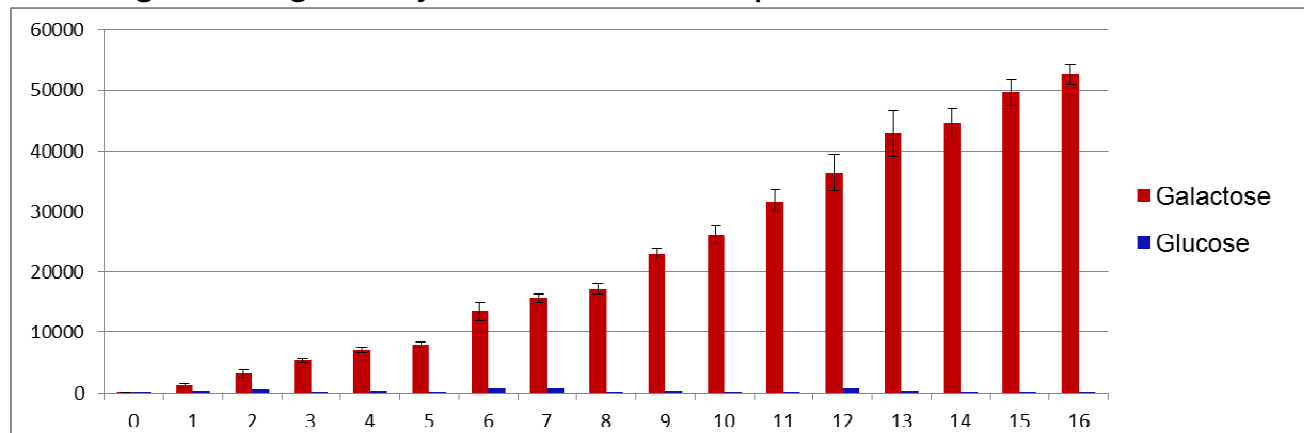
Largest library of promoters in *Y. lipolytica*



Strongest constitutive promoter in *S. cerevisiae*



Largest range of synthetic inducible promoters in *S. cerevisiae*

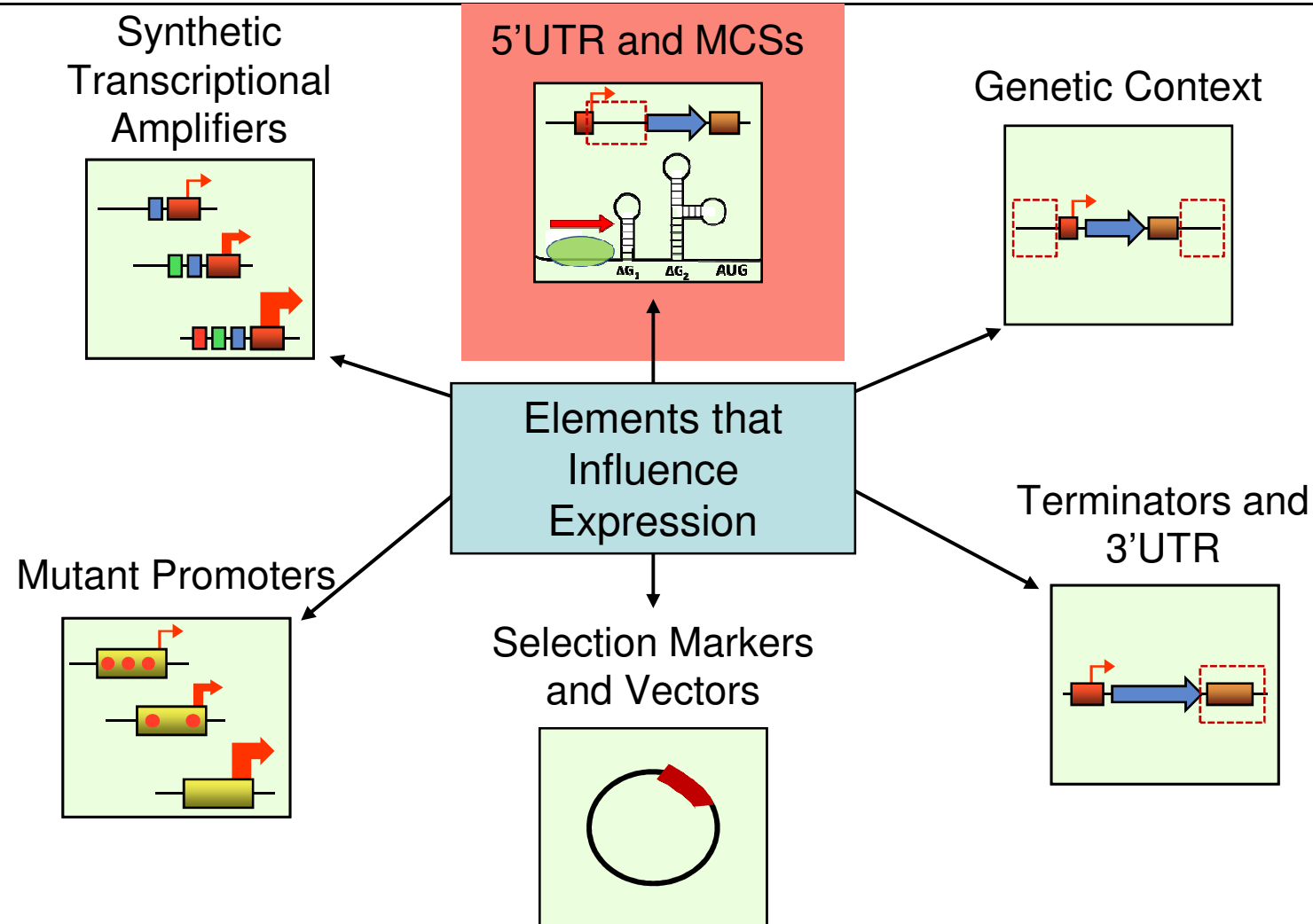


Blazeck et al., *AEM*, 77(22), 2011 & Blazeck et al., *Accepted/In Press, Biotech Bioeng*, 2012

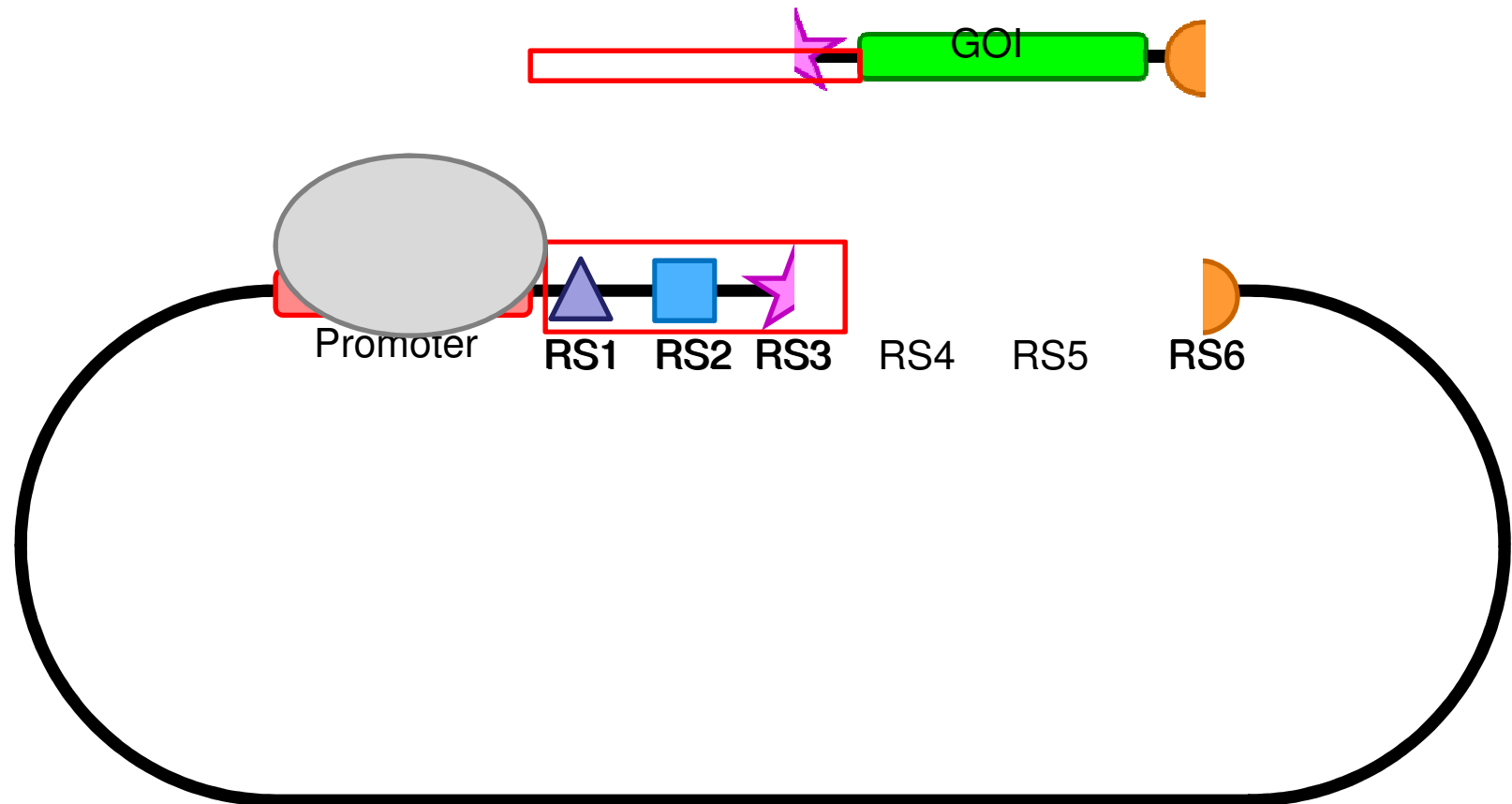
Synthetic, hybrid promoters

- UAS elements serve as synthetic transcriptional amplifiers
- UAS elements and core promoters can serve as modular synthetic components
- Hybrid promoter engineering can amplify expression and create highly-functional libraries

Synthetic control of transcription occurs at many levels



Multicloning sites influence 5'UTR sequences



Crook et al., *Nucleic Acids Research*, 39(14), e92, 2011

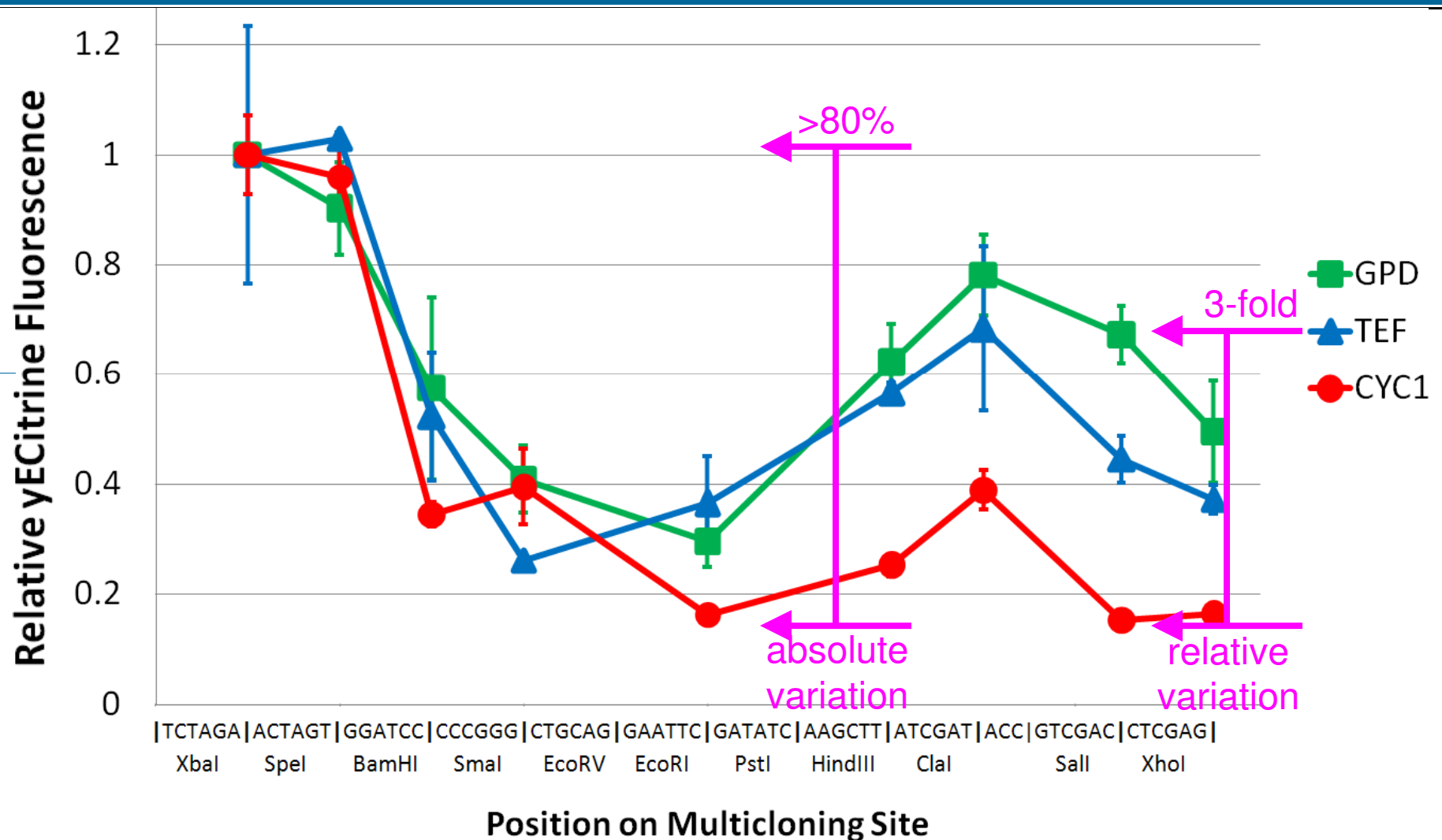
Model System

- Yeast model system (*S. cerevisiae*)
- pBluescript SK II Multicloning Site

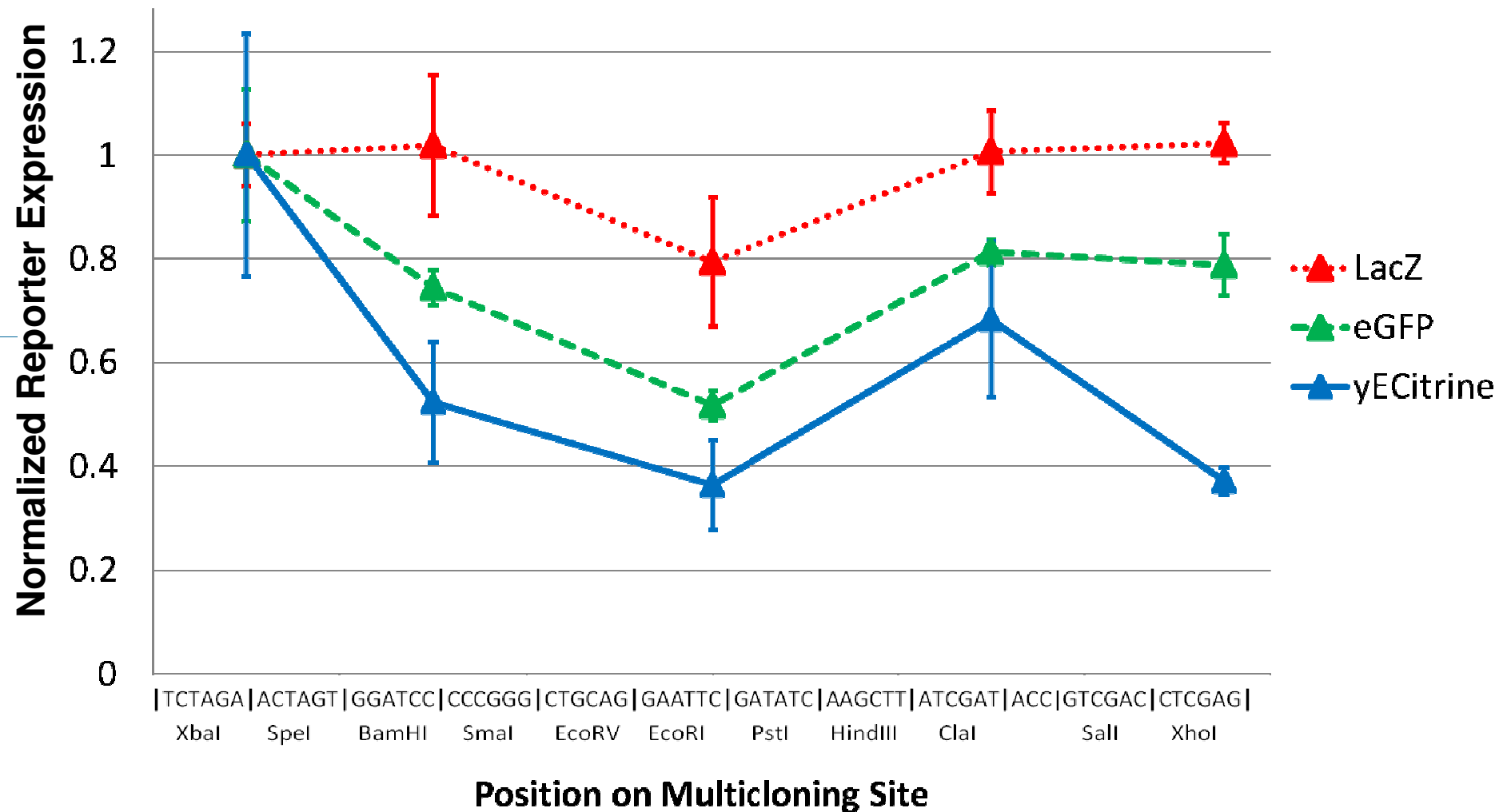
|TCTAGA|ACTAGT|GGATCC|CCCGGG|CTGCAG|GAATTC|GATATC|AAGCTT|ATCGAT|ACC|GTCGAC|CTCGAG|
XbaI SpeI BamHI SmaI EcoRV EcoRI PstI HindIII ClaI SalI XhoI

- CYC1, TEF, or GPD promoters
- yECitrine
 - Codon-optimized

Restriction site affects protein expression

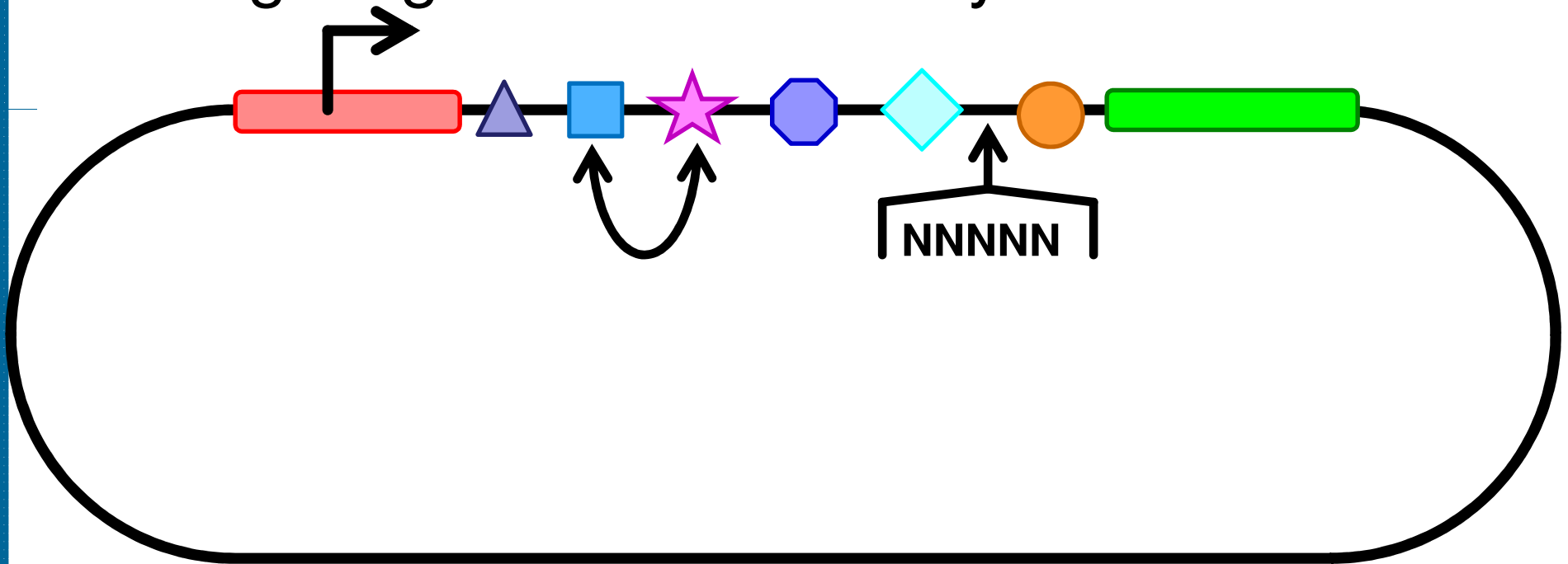


Effect is most pronounced with short, codon-optimized genes



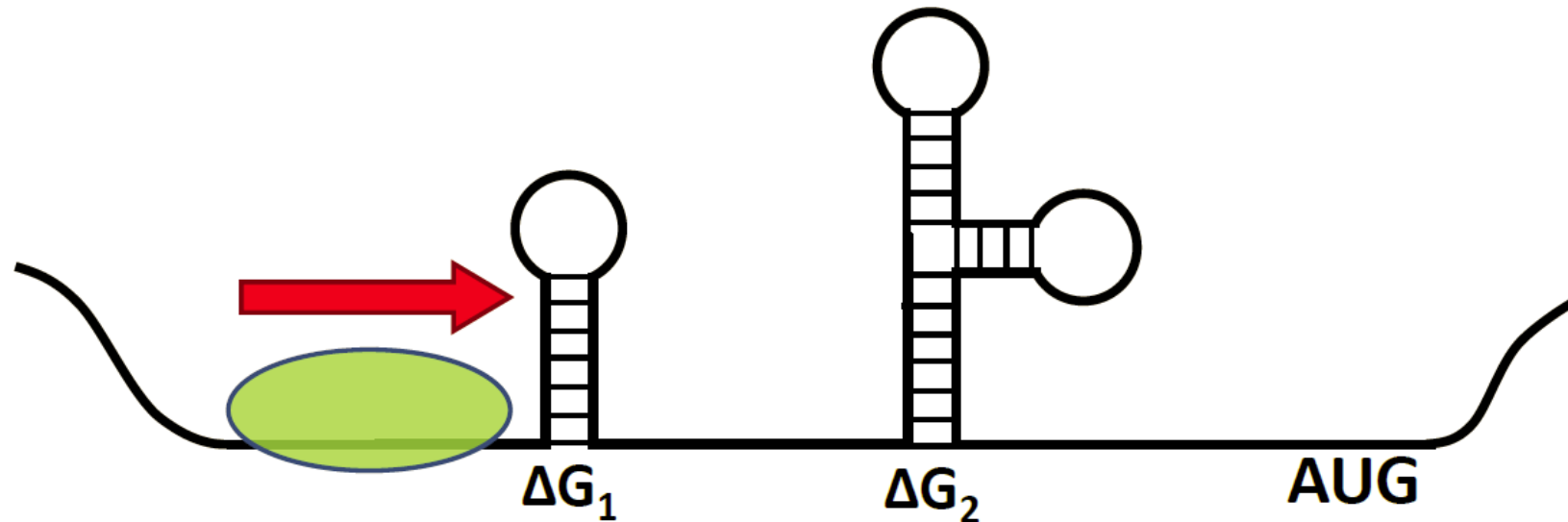
Modeling and re-designing MCSs

- Goal: Use model to re-design better MCSs not susceptible to position effect by mitigating 5'UTR secondary structure

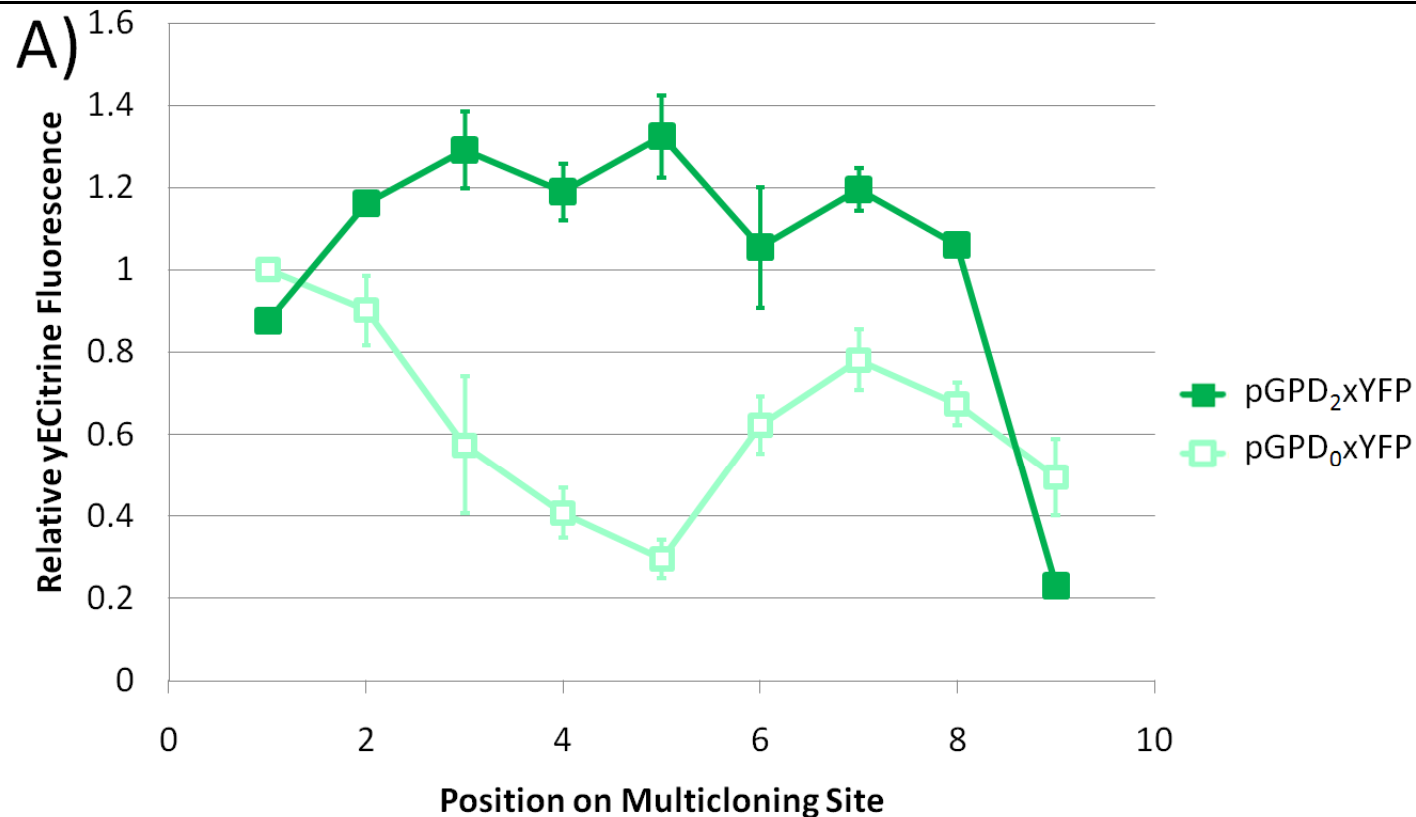


Conceptual model of inhibition

- Region(s) of secondary structure in 5'UTR can impede ribosome progression



Modeling and re-designing MCSs: GPD/TDH3-based Promoter



|TCTAGA|ACTAGT|GGATCC|CCCGGG|CTGCAG|GAATTC|GATATC|AAGCTT|ATCGAT|ACC|GTCGAC|CTCGAG|
XbaI 1 SpeI 2 BamHI 3 XmaI 4 PstI 5 EcoRI 6 EcoRV 7 HindIII 8 ClaI 9 SalI 10 XhoI 11

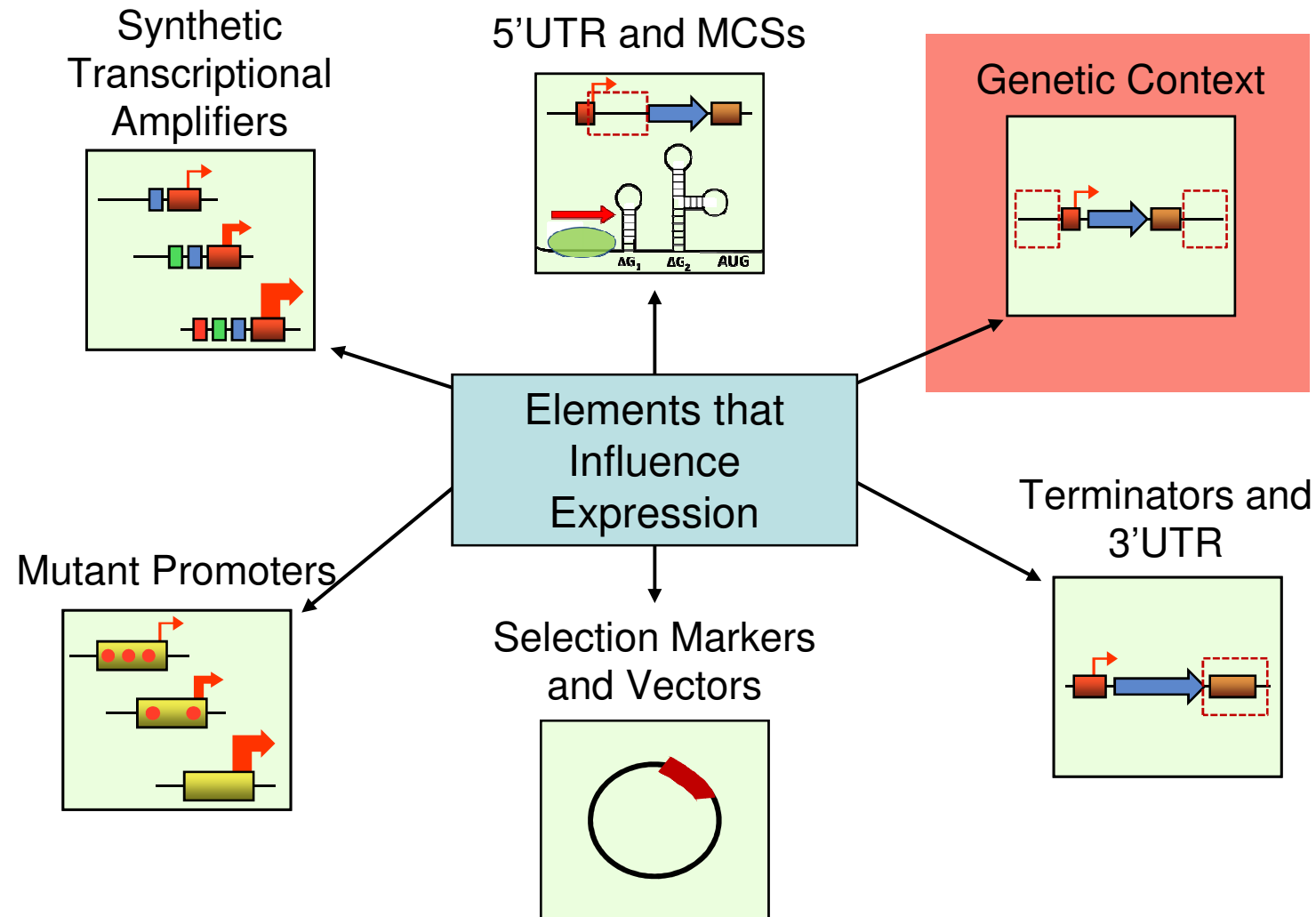
|A|AAGCTT|ACTAGT|ATCGAT|AAA|GAATTC|TCTAGA|GGATCC|CTGCAG|CTCGAG|GTCGAC|CCCGGG|GATATC|
HindIII 1 SpeI 2 ClaI 3 EcoRI 4 XbaI 5 BamHI 6 PstI 7 XhoI 8 SalI 9 XmaI 10 EcoRV 11

Crook et al., *Nucleic Acids Research*, 39(14), e92, 2011

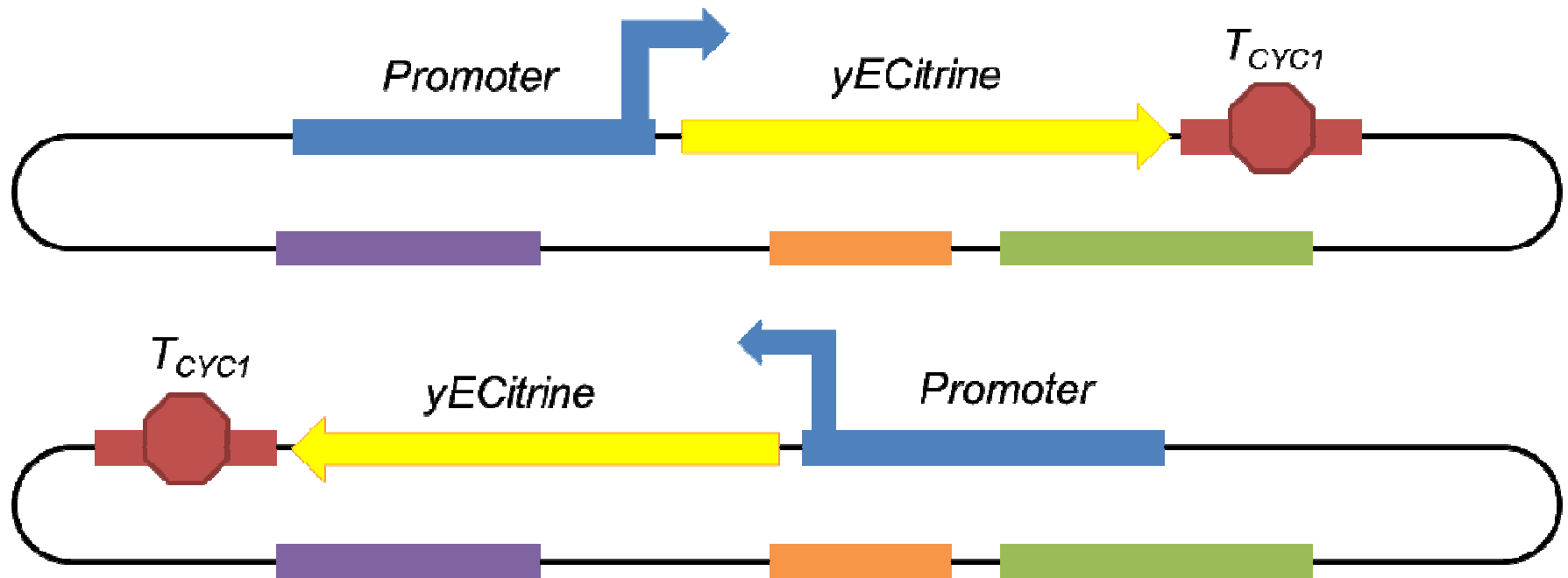
5'UTR Influence

- Choice of site in MCS can influence 5'UTR regions via secondary structure
- Most pronounced by short, codon-optimized genes (i.e. when transcription and translation rates are not limiting)
- Can use model-based approach to improve MCS design (esp. with GPD)
- Genetic context is important for characterizing parts

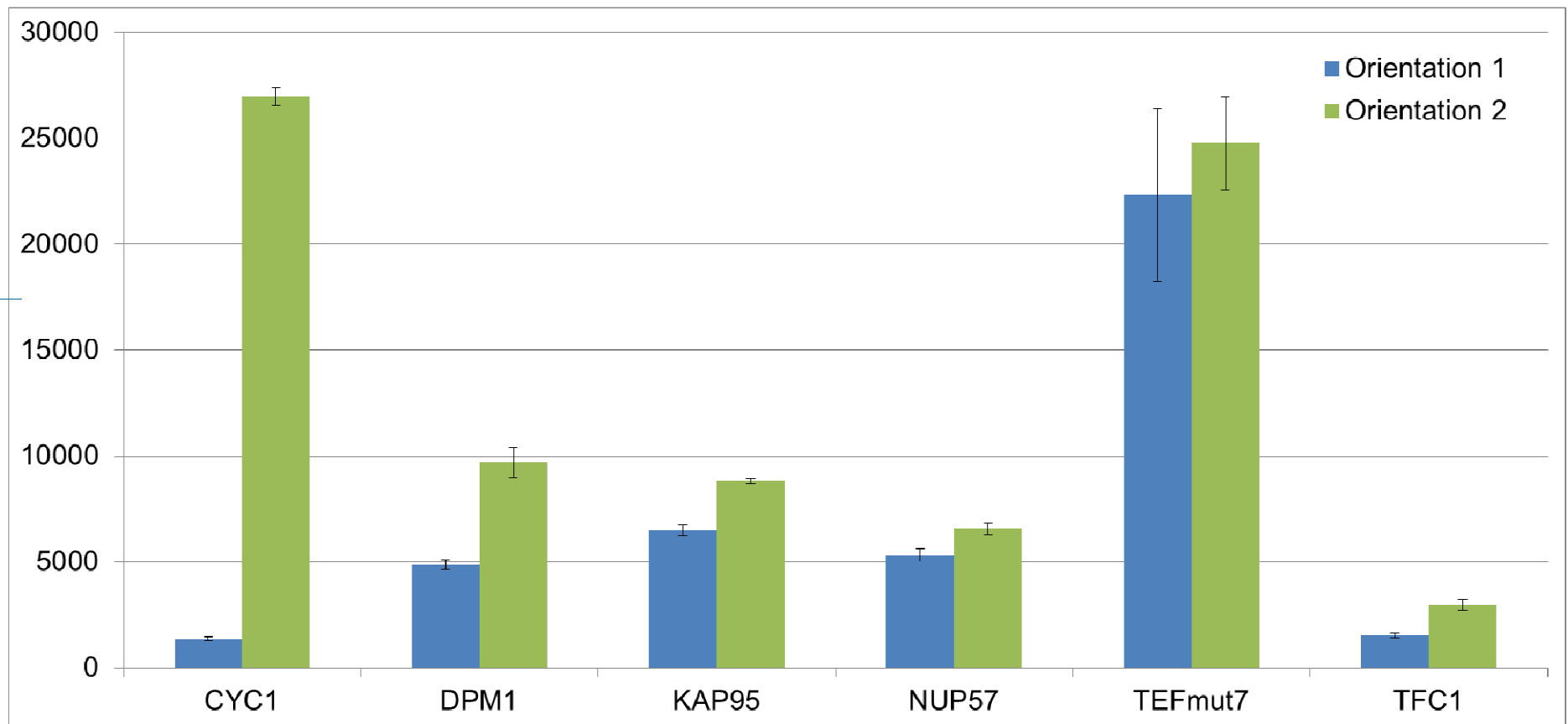
Synthetic control of transcription occurs at many levels



Importance of genetic context



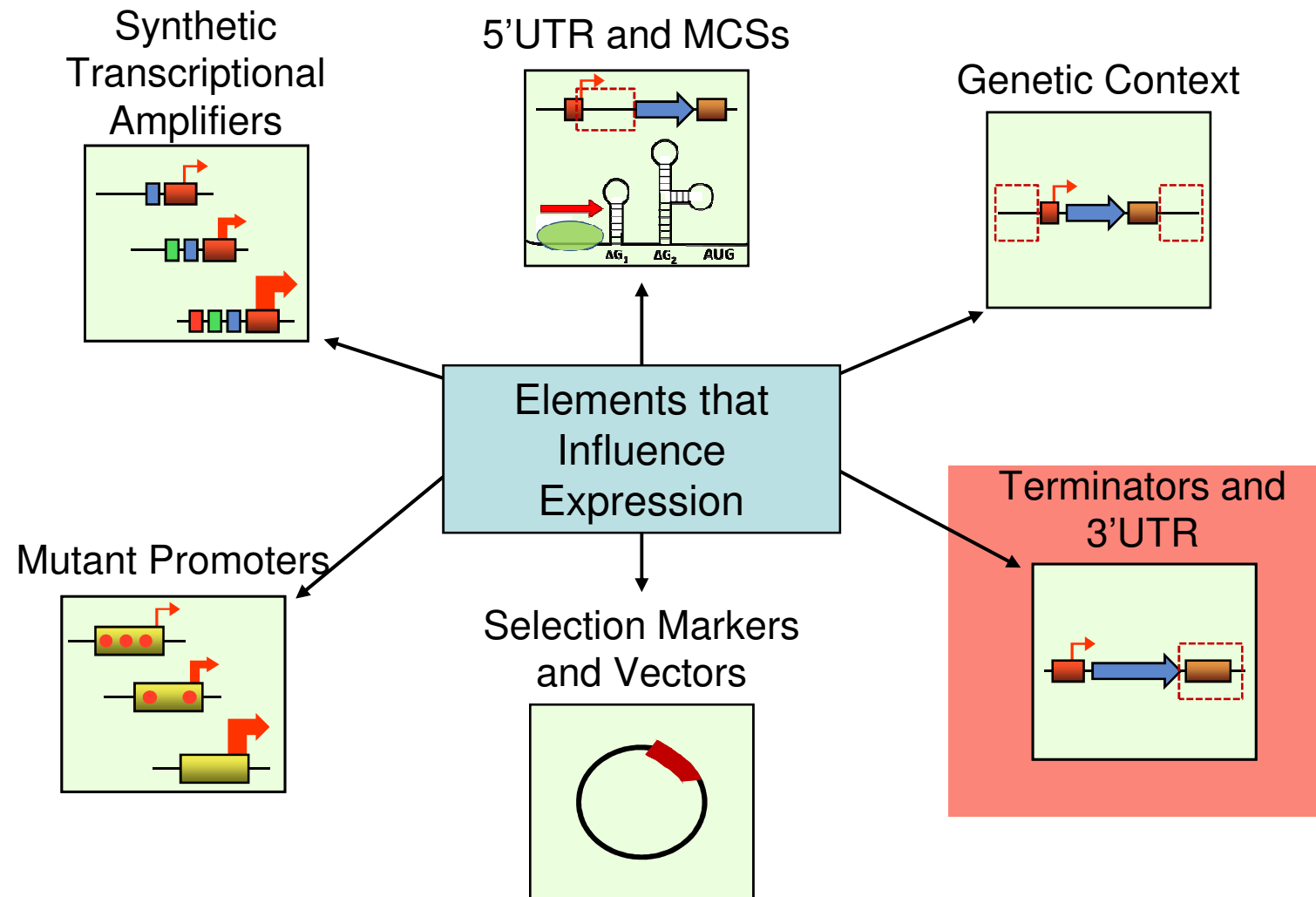
Importance of genetic context



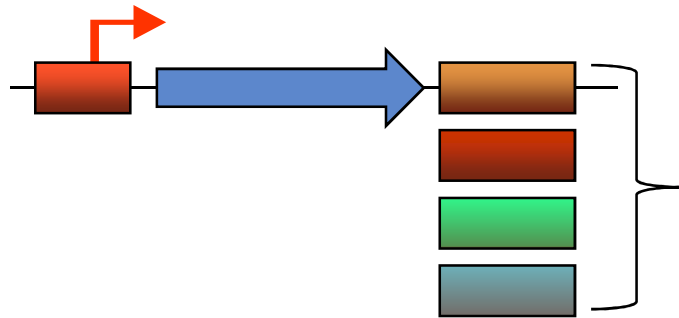
Genetic Context

- Results highlight importance of genetic context of synthetic parts
 - Plasmids vs. genomic integration site
- Highlight need for insulating elements

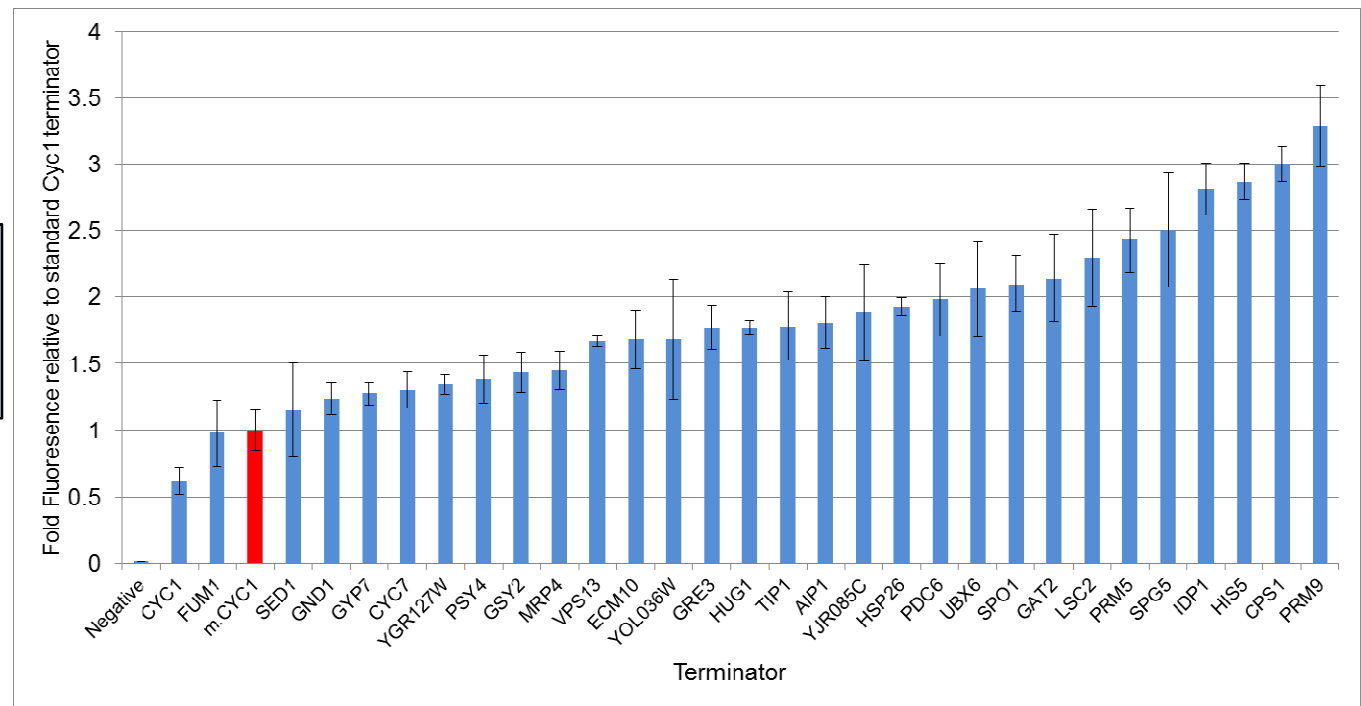
Synthetic control of transcription occurs at many levels



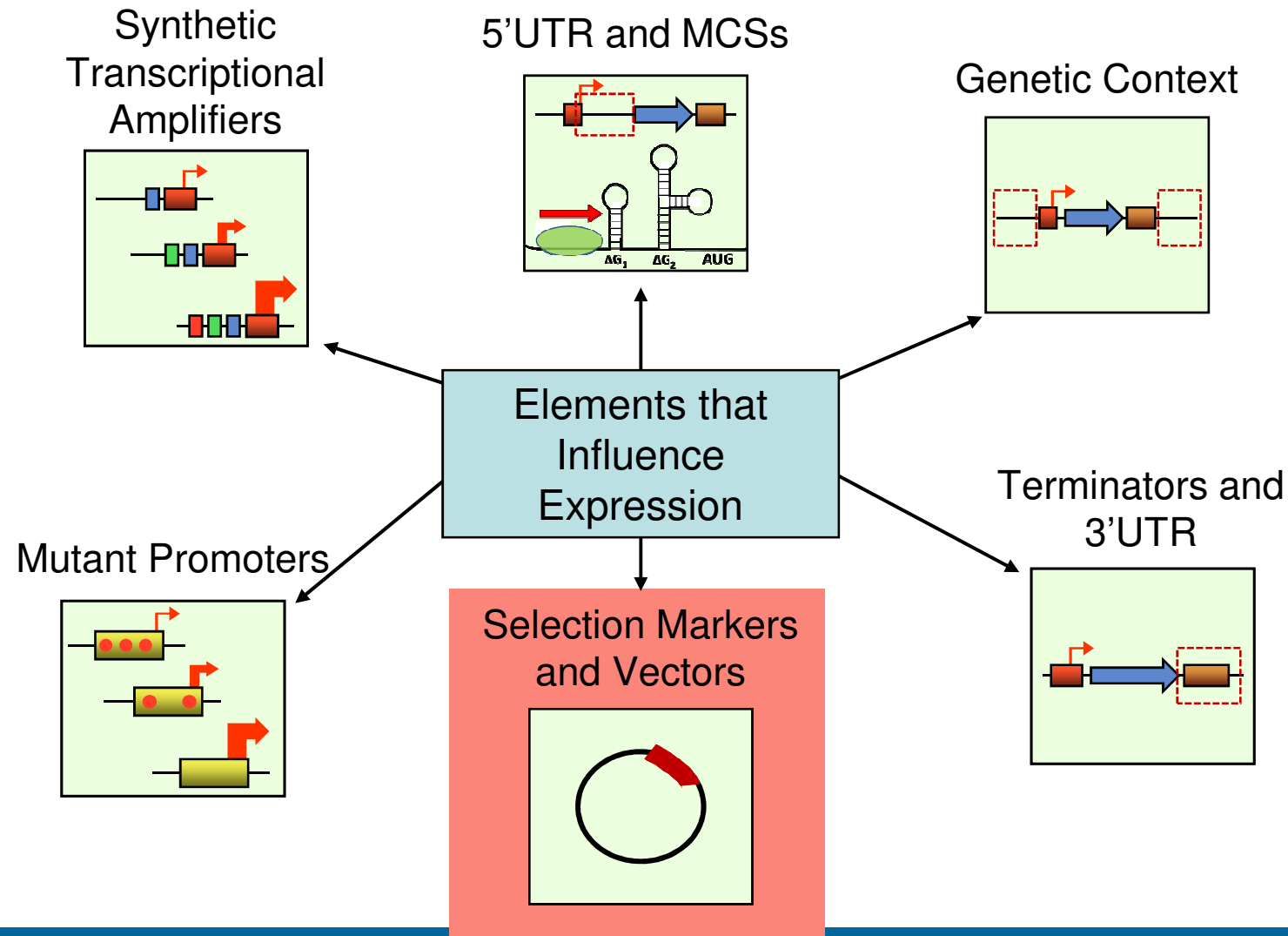
Terminator choice can influence performance



>5 fold difference in expression output by changing terminator



Synthetic control of transcription occurs at many levels



Final Thoughts

- Synthetic control elements are a critical tool for implementing M.E. strategy
- “Promoters” cannot be thought of as singular, isolated elements
- Currently require slightly more range, but significantly more sequence diversity
- Starting to understand fundamental design principles for these critical components
- These elements are greatly enhancing our capacity to metabolically engineer pathways

Acknowledgements



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Heming Bai

Alex Bailey

Austin Comer

Tim Dyess

Rishi Garg

Rachelle Gerstner

Akash Gupta

Daniel Huang

Taylor Jellison

Ashty Karim

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Annie Pan

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Ben Reed

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Andrea Zuzack



Laboratory for Cellular
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Hal Alper

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Slide # 41